OCT 1 0 2000 A PADEMARY

SEQUENCE LISTING

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<110> Kilian, Andrzej
      Bowtell, David
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<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES THEREOF

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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu

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Leu Ala Phe Gy Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val

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Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg 225 230 230 240

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Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr\Ser Leu Glu Gly Ala 275 280 285

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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 335

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Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His

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My Hars

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695

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Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
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Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu 850 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala 865 870 875 880

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Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu 900 905 \uparrow 910

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Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe 945 950 955 $\sqrt{}$ 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly 965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn 980 985

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln

Herry

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Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys 65 70 75

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
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Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu 115 120 125

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Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Lys Lys 245 250 255

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J. Zus

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Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr 595 600

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M. A.

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Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val 945 950 960

Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile 965 970 975

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JUNE N

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Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala 565 570 575

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Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser 725 730 735

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Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
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N. K.

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Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val

Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn 65 70 75 80

Val Leu Thr Phe G Λ y Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn 90 95

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val

Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe 130 140

Thr Gln Ile Val Gly Asn Arg Sys Asn Glu Pro His Leu Pro Pro Lys
145 150 155 160

Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys 165 170 175

Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn 180

Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser 195 200 205

Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr 210 220

Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr 225 230 235

Leu Gln Lys Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
245 250 250

Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser 260 265 270

His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile 275

Val Ile Leu Gln Lys Leu Pro Gln Glu Met Phe Gly Ser Lys Lys 290 295

Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu 305 310 315

Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu

A M

330 335 Lys Aspigg
anglePhe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His Asn Phe G 1μ Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu Phe Arg Gln $ar{m{\lambda}}$ eu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser SerackslashThr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp 390 395 Asn Lys Leu Ile Th Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu Val Glu Asn Asn Val lphays Arg Asn His Asn Ser Tyr Thr Leu Ser Asn 425 Phe Asn His Ser Lys MetackslashArg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Phe Thr Ile Tyr Lys Glu Asn His L vs Asn Ala Ile Gln Pro Thr Gln Lys 470 475 Ile Leu Glu Tyr Leu Arg Asn Lys \sqrt{A} rg Pro Thr Ser Phe Thr Lys Ile 490 509 Leu Leu Lys Lys Phe Asn Asn Val Leu Rro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met 530 535 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Aan Gly Phe Phe Val Arg Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn 570 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu\Leu Tyr Ile Asp Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile

625 630 635 640 Val Asp Le $oldsymbol{\chi}$ Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys 650 Ala Ser Pro Sè χ Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe 665 Leu Ile Ile Ser The Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu 680 Ala Met Gly Gly Phe $\delta \chi$ n Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala Val Ser Ser In Ser Asp Asp Thr Val Ile Gln Phe 710 715 Cys Ala Met His Ile Phe ValigglaubleLys Glu Leu Glu Val Trp Lys His Ser Ser Thr Met Asn Asn Phe His Il $m{k}$ Arg Ser Lys Ser Ser Lys Gly Ile 745 Phe Arg Ser Leu Ile Ala Leu Phe Arg Thr Arg Ile Ser Tyr Lys Thr 760 Ile Asp Thr Asn Leu Asn Ser Thr Asn $\sqrt{ ext{Thr}}$ Val Leu Met Gln Ile Asp 775 His Val Val Lys Asn Ile Ser Glu Cys Ty χ Lys Ser Ala Phe Lys Asp Leu Ser Ile Asn Val Thr Gln Asn Met Gln Ahe His Ser Phe Leu Gln 805 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro\Ile Thr Lys Cys Asp Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Le $oldsymbol{\psi}$ Asn Gly Phe Leu Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Vle Tyr Ile His Ile Val Asn <210> 6 <211> 13 <212> DNA <213> Homo sapiens

MAN

<220>

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  <400> 6
  ccaggtgggc ct
                                                                       13
  <210> 7
  <211> 14
  <212> DNA
  <213> Homo sapien
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 <221> intron
 <222> (1)..(7)
 <223> Last seven bases\setminusof intron Y
 <400> 7
 gcaggtgtcc tgcc
                                                                       14
 <210> 8
 <211> 14
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron 1
 <400> 8
aaagagggtg gctg
                                                                      14
<210> 9
<211> 14
<212> DNA
<213> Homo sapiens
<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron 1
<400> 9
aacagaagcc gagc
                                                                    14
<210> 10
<211> 14
<212> DNA
<213> Homo sapiens
<220>
<221> intron
<222> (8)..(14)
<223> First 7 bases of Intron Alpha
<400> 10
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tgtcaagg gatg
                                                                       14
 <210> 11
 <211> 14
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron Alpha
 <400> 11
 ccccaggac aggc
                                                                      14
 <210> 12
 <211> 14
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> intron
 <222> (8)..(14)
 <223> First 7 bases of Intron Beta
 <400> 12
 gagccacgtc tcta
                                                                      14
 <210> 13
 <211> 14
<212> DNA
<213> Homo sapiens
<220>
<221> intron
<222> (1)..(7)
<223> Last 7 bases of Intron Beta
<400> 13
ggggcaagtc ctac
                                                                     14
<210> 14
<211> 14
<212> DNA
<213> Homo sapiens
<220>
<221> intron
<222> (8)..(14)
<223> First 7 base of Intron 2
<400> 14
actccaggtg agcg
                                                                     14
<210> 15
<211> 14
<212> DNA
```

KW

```
<213> Homo sapiens
  <220>
  <221> moditied_base
  <222> (1)..\7)
  <223> Wherei\hbar N is any nucleotide
 <220>
 <221> intron
 <222> (1)..(7)
 <223> Last 7 bases of Intron 2
 <400> 15
 nnnnnncta tgcc
                                                                      14
 <210> 16
 <211> 173
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> intron
 <222> (8)..(166)
 <223> Full Sequence of Intron\3
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 gagatggage cacecegeag accgtegggt tggggeaget tteeggtgte teetgggagg 120
 ggagttgggc tgggcctgtg actecteage coctgtttte ceceagggat gte
 <210> 17
 <211> 46
 <212> PRT
<213> Homo sapiens
<400> 17
Thr Ala Ala Glu Glu Asn Ile Leu Val Val Th\chi Pro Ala Val Leu Gly
Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly
                                   25
Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu\sqrt{G}ly Leu
                              40
<210> 18
<211> 104
<212> DNA
<213> Homo sapiens
<220>
<223> Intron Y
<400> 18
ggcctccccg gggtcggcgt ccggctgggg ttgagggcgg ccggggggaa ccagcgecat 60
geggagagea gegeaggega eteagggege tteeceegea ggtg
```

```
<210> 19
 <211> 34
 <212> PRT
 <213> Homo\sapiens
 <220>
 <223> Reding Rrame One of Intron Y
 <400> 19
 Gly Leu Pro Gly \sqrt[\Lambda]{q}l Gly Val Arg Leu Gly Leu Arg Ala Gly Gly
 Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro
 Arg Arg
 <210> 20
 <211> 10
 <212> PRT
 <213> Homo sapiens
<220>
<223> Reading Frame Two of Intron\backslashY before termination
       Codon
<400> 20
Ala Ser Pro Gly Ser Ala Ser Gly Trp 🎝
<210> 21
<211> 23
<212> PRT
<213> Homo sapiens
<220>
<223> Reading Frame Two of Intron Y after termination
      Codon
<400> 21
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ata Gln Ala Thr
Gln Gly Ala Ser Pro Ala Gly
<210> 22
<211> 34
<212> PRT
<213> Homo sapiens
<220>
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<223> Reading Frame Three of Intron Y
 <400> 22
 Pro Pro Arg Cly Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu
 Pro Ala Thr Cys Qly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro
 Gln Val
 <210> 23
 <211> 38
 <212> DNA
 <213> Homo sapiens
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 <223> Intron 1
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gtggctgtgc tttggtttaa cttccttttt aaccagaa
                                                                    38
<210> 24
<211> 13
<212> PRT
 <213> Homo sapiens
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<223> Intron 1 Translation
<400> 24
Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys
<210> 25
<211> 36
<212> DNA
<213> Homo sapiens
<220>
<223> Intron Alpha
<400> 25
gtggatgtga cgggcgcgta cgacaccatc ccccaq
                                                                    36
<210> 26
<211> 12
<212> PRT
<213> Homo sapiens
<220>
<223> Intron Alpha Translation
<400> 26
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Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln
   1
 <210> 27
 <211> 182
 <212> DNA
 <213> Homo sapiens
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 <400> 27
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accagecege tgagggatge\egteqteate gageagaget cetecetgaa tgaggecage 120
agtggcetet tegaegtett actaegette atgtgecace acgeegtgeg cateagggge 180
<210> 28
<211> 61
<212> PRT
<213> Homo sapiens
<220>
<223> Intron Beta Translation
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Val Ser Thr Leu Thr Asp Leu Gln Pr\sim Tyr Met Arg Gln Phe Val Ala
His Leu Gln Glu Thr Ser Pro Leu Arg \lambdasp Ala Val Val Ile Glu Gln
              20
Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly\backslashLeu Phe Asp Val Phe Leu
Arg Phe Met Cys His His Ala Val Arg Ile Ar\c A Gly Lys
<210> 29
<211> 226
<212> DNA
<213> Homo sapiens
<220>
<223> Intron 2
<400> 29
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cegttgegte caeetetget teegtgtggg geaggegaet geeaateeea aaggeteaga 120
tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcatctt tctgtgggag 180
tgagggtgcc tcacaacggg agcagttttc tgtgctattt tggtaa
                                                                     226
<210> 30
<211> 159
<212> DNA
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<213>\Homo sapiens
 <220>
 <223> Intron 3
 <400> 30
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 ccgaagaaaa'
 agécaccecg agacegieg ggigtgggga géittecggi gtetéétggg aggggagtig 120
 ggctgggcct gtgactcctc agcctctgtt ttcccccag
 <210> 31
 <211> 44
 <212> PRT
 <213> Homo sapiens
 <220>
 <223> Intron 3 Translation
 <400> 31
 Ala Glu Glu Asn Ile Ser ^{\lambda} al Val Thr Pro Ala Val Leu Gly Ser Gly
 Gln Pro Glu Met Glu Pro Pro Arg Pro Ser Gly Val Gly Ser Phe
 Pro Val Ser Pro Gly Arg Gly Val \cVent{V}ly Leu Gly Leu
 <210> 32
 <211> 262
 <212> DNA
<213> Homo sapiens
<220>
<223> Intron X. Complete length unknown
<400> 32
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ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gt tggctgg catgggtgga 120
cgtggccccg ggcatggcct tetgcgtgtg ctgccgtggg tgcctgagc cctcactgag 180
tcggtggggg cttgtggctt cccgtgagct tccccctagt ctgt gtctg gctgagcaag 240
cctcctgagg ggctctctat tg
                                                                     262
<210> 33
<211> 218
<212> DNA
<213> Homo sapiens
<220>
<223> Partial Sequence of Genomic Intron (approximately
      2.7 \text{ kb}
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gtatcagett agatgaaggg eeeggaggag gggeeaeggg acaeageeag ggeeatgg\deltaa 120
cggcgcccac ccatttgtgc gcacagtgag gtggccgagg tgccggtgcc tccagaaaa 180
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```
cagcqtgggg gtgtaggggg agctcctggg gcagggac
                                                                     218
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 <211> 2031
 <212> DNA
 <213> Hono sapiens
 <220>
 <221> modified_base
 <222> (1767)\. . (1769)
 <223> Wherein N is A, C, G or T
 <220>
 <223> N-Terminaar{m{1}} Truncated Telomerase
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 egeggggace eggeggett cegegegetg gtggeecagt geetggtgtg egtgeectgg 180
 gacgeaegge egeceeeg\lambda egeceetee tteegeeagg tgteetgeet gaaggagetg 240
 gtggcccgag tgctgcagag \gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300
 ttegegetge tggaegggge &eceeegagg cetteaceae eagegtgege 360
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 ctgcgccgcg tgggcgacga cg gctggtt cacctgctgg cacgctgcgc gctctttgtg 480
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gccactcagg cccggcccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600
cgggcctgga accatagcgt cagggqcc ggggtccccc tgggcctgcc agccccgggt 660
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ggcgctgccc ctgagccgga gcggacgcc gttgggcagg ggtcctgggc ccacccgggc 780
aggacgegtg gacegagtga cegtggtte tgtgtggtgt cacetgecag accegecgaa 840
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gtggagacca tetttetggg ttecaggeee t\sqrt[6]{g}atgeeag ggaeteeeg eaggttgeee 1140
egeetgeece agegetactg geaaatgegg ce\deltaetgttte tggagetget tgggaaceae 1200
gegeagtgee cetaeggggt geteeteaag acgaetgee egetgegage tgeggteace 1260
ccagcagecg gtgtetgtge eegggagaag eeceaggget etgtggegge eecegaggag 1320
gaggacacag accecegteg cetggtgeag etget\delta_{
m c}gec ageacageag eccetggeag 1380
gtgtacgget tegtgeggge etgeetgege eggetggtge eeceaggeet etggggetee 1440
aggeacaaeg aacgeegett eeteaggaae accaagaagt teateteeet ggggaageat 1500
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ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740
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tgccgtgggt gccctgagcc ctcactgagt cggtgggggc ttgtggcttc ccgtgagctt 1980
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<212> PRT
<213> Homo sapiens
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

Ala Leu Val Ala Gla Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu 65

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val

Leu Ala Phe Gly Phe Ala Leu Asp Gly Ala Arg Gly Gly Pro Pro

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr 115 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro His Ala Ser Gly 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg 195 200

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg 225 230 235

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp 245 250

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cyc Val

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala 275

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 330 335

Asp Lys Glu Gin Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln 370 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 385 390 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu 435

Val Gln Leu Leu Arg Gln His Ser $\begin{array}{c} \text{Ser} \\ \text{450} \end{array}$ For Pro Trp Gln Val Tyr Gly Phe

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met 500 505

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Set Pro Gly Val Gly Cys 515 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ne Leu Ala Lys Phe 530 535

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe 555 550

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Let Phe Phe Tyr 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly 580

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gegeagtgee cetaeggggt geteeteaag acgeatgee egetgegage tgeggteace 1260
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aggeacaaeg aaegeegett eeteaggaae accaagaagt teateteeet ggggaageat 1500
gccaagetet egetgeagga getgaegtgg aagatgag\partial_{q} tgegggaetg egettggetg 1560
egeaggagee caggggttgg etgtgtteeg geegeagag\Deltaacegtetgeg tgaggagate 1620
ctggccaagt teetgeactg getgatgagt gtgtacgteg tegagetget caggtettte 1680 ttttatgtea eggagaceae gttteaaaag aacaggetet tettetaeeg gaagagtgte 1740
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aaccagaage egagegtete acetegaggg tgaaggcact gttcagegtg etcaactacg 2040
                                                                       2041
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<211> 670
<212> PRT
<213> Homo sapiens
<220>
<223> Truncated Protein 1; Encoded by SEQ ID NO:36
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

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Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 295 300

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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 330 335

Asp Lys Glu Gan Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Leu Pro Arg Leu Pro Gln 370 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 390 395 400

Ala Gln Cys Pro Tyr Gly Wal Leu Leu Lys Thr His Cys Pro Leu Arg

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Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu 435

Val Gln Leu Leu Arg Gln His Ser $\begin{array}{c} \text{Ser} \\ \text{450} \end{array}$ For Pro Trp Gln Val Tyr Gly Phe

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Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser

Leu Gly Lys His Ala Lys Leu Ser Leu Gln $\begin{tabular}{lll} \begin{tabular}{lll} \begin{tabular} \begin{tabular}{lll} \begin{tabular}{lll} \begin{tabular$

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Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 300

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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325

Asp Lys Glu Gln Leu Arg Pro Ser\Phe Leu Leu Ser Ser Leu Arg Pro 340 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355

Arg Pro Trp Met Pro Gly Thr Pro Arg Leu Pro Arg Leu Pro Gln 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 385 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu 435

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe 450 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser 470 475

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Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 530 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe 555 550 560

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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 340 350

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Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 385 390 395

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Leu Gly Lyk His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met 500 505 510

Ser Val Arg Arp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys 515 520 525

Val Pro Ala Ala Clu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 530 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe 545 550 555 560

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Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg 660 670

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Pro Pro Ala Ala Aro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu 65 70 75 80

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Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro His Ala Ser Gly
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Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 295 300

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Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 340 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355 360 365

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Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 390 395 400

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Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu 435

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
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Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser 490 495

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Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Rhe 545 550 555

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Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val 625 630 635 640

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Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg 660 665 670

Pro Gly Leu Neu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro 690 695 700

Glu Leu Tyr Phe Val Dys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
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Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His 740 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
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Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser 770 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gla Ser Ser Ser Leu Asn Glu 785 790 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro 820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu 850 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala 865 870 875

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys 885 890 895

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Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe 915 920 925

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Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 295 300

Ala Gly Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 330 335

Asp Lys Glu Gln Led Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 340 350

Ser Leu Thr Gly Ala Ary Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355 360 365

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Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His 385 390 400

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Ala Ala Val Thr Pro Ala Ala Gly Val Sys Ala Arg Glu Lys Pro Gln 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe 450 455

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser 470 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe 545 550 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr 565 570 575

Akg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His 580 590

Leu Leu Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser 645 650 655

Arg Val Lys Ala Leu Ahe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro 690 700

Glu Leu Tyr Phe Val Lys Asp Ard Leu Thr Glu Val Ile Ala Ser Ile
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Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
725 730 735

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser 740 750

Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg G n Phe Val Ala His Leu 755 760 765

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser 770 775 780

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe 790 795 800

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr \upgamma_{805} Gln Cys 810

Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu 820 825 830

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp 835 840 845

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro 865 870 875 880

Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro 885 890 895

Val Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala 900 905 910

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu 925

Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala 930 935 940

Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg 945 950 955 960

Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp 965 970 975

Leu Gln Val Asn Ser Leb Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
980 985 990

Leu Leu Gln Ala Tyr Ang Phe His Ala Cys Val Leu Gln Leu Pro 995 1000 1005

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile 1010 1015 1020

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala 1025 1030 1040

Gly Met Ser Leu Gly Ala Lys Gly Ala Gly Pro Leu Pro Ser Glu 1045 1050 1055

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1060 1065 1070

His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln 1075 1080 1085

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr $\frac{1}{1000}$ Thr Ala Leu Glu $\frac{1090}{1000}$

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<220>

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Beta and 2

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35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu 65 70 75 80

Val Ala Arg Val Leu Gln Arg Yeu Cys Glu Arg Gly Ala Lys Asn Val 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Pro Pro 100 110

Glu Ala Phe Thr Thr Ser Val Arg Set Tyr Leu Pro Asn Thr Val Thr 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val 145 150 150

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly

Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg 230 235 230 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val

260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His 290 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly 325 330 335

Asp Lys Glu Gln Lev Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser 355 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Leu Pro Arg Leu Pro Gln 370 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His-385 390 400

Ala Gln Cys Pro Tyr Gly Val Leu Lys Thr His Cys Pro Leu Arg
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Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln 420 425

Gly Ser Val Ala Ala Pro Glu Glu Glu Aso Thr Asp Pro Arg Arg Leu 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe 450 455

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Cly Leu Trp Gly Ser

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr $\frac{1}{500}$ Lys Met $\frac{1}{500}$

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe 550 550 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr

X

565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His 580 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln 605

His Arg Glv Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val 625 630 635 640

Gly Ala Arg Thr the Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg 660 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
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Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
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Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Gln
725 730 735

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser 740 750

Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu 755 760 765

Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser 770 775 780

Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe 785 790 795 800

Met Cys His His Ala Val Arg Ile Arg Gly Lys Sex Tyr Val Gln Cys 805 810 815

Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu 820 825

Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp 835

Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His 850 860

Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val

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870
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         35
                                                 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp\ Asp Ala Arg Pro
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Lev Lys Glu Leu
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Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Las Asn Val
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro
            100
                                                   110
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
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115 120 125 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val 135 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val 150 Leu Val\Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gl Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly 185 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Aro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser 🎠 rg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro\Glu Arg Thr Pro Val Gly Gln Gly Ser Trp 245 Ala His Pro Gly Arg Thr Ara Gly Pro Ser Asp Arg Gly Phe Cys Val 265 Val Ser Pro Ala Arg Pro Ala G $ho_{\!\!
m L}$ Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His P χ o Ser Val Gly Arg Gln His His 295 Ala Gly Pro Pro Ser Thr Ser Arg Pro Arg Pro Trp Asp Thr Pro 315 Cys Pro Pro Val Tyr Ala Glu Thr Lys His The Leu Tyr Ser Ser Gly 330 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile\Phe Leu Gly Ser 360 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln 375

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
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Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gli Asn His

390

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln

420 425 430

Glv Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu 435

Val Gln Leu Leu Arg Gln His Asp Ser Ser Pro Trp Gln Val Tyr Gly Phe 450

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser 470

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser 490

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met 500

Ser Val Arg Asp Asp Cys Ala Trp Leu Arg Arg Arg Ser Pro Gly Val Gly Cys

Val Pro Ala Ala Glu Ais Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe 530 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe 545 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr 565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His 580 590

Leu Lys Arg Val Gln Leu Arg Glu Deu Ser Glu Ala Glu Val Arg Gln 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile 610 615

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val 625 630 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Gla Arg Ala Arg Arg 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro 690 695 700

Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile 705 710 715

Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln

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Gln	Gly	Ile	Pro 820	Gln	Gly	Ser	Ile	Leu 825	Ser	Thr	Leu	Leu	Cys 830	Ser	Leu
Cys	Tyr	Gly 835	Asp	Met	Glu	Asn	Lys 840	Leu	Phe	Ala	Gly	Ile 845	Arg	Arg	Asp
Gly	Leu 850	Leu	Leu	Arg	Leu	Val 855	Asp	Asp	Phe	Leu	Leu 860	Val	Thr	Pro	His
Leu 865	Thr	His	Ala	Lys	Thr 870	Phe	Leu	Arg	Thr	Leu 875	Val	Arg	Gly	Val	Pro 880
Glu	Tyr	Gly	Cys	Val 885	Val	Asn	Leu	Arg	Lys 890	Thr	Val	Val	Asn	Phe 895	Pro
Val	Glu	Asp	Glu 900	Ala	Leu	Gly	Gly	Thr 905	Ala	Phe	Val	Gln	Met 910	Pro	Ala
His	Gly	Leu 915	Phe	Pro	Trp	Cys	Gly 920	Leu	Leu	Leu	Asp	Thr 925	Arg	Thr	Leu
Glu	Val 930	Gln	Ser	Asp	Tyr	Ser 935	Ser	Tyr	Ala	Arg	Thr 940	Ser	Ile	Arg	Ala
Ser 945	Leu	Thr	Phe	Asn	Arg 950	Gly	Phe	Lys	Ala	Gly 955	Arg	Asn	Met	Arg	Arg 960
Lys	Leu	Phe	Gly	Val 965	Leu	Arg	Leu	Lys	Cys 970	His	Ser	Leů	Phe	Leu 975	Asp
Leu	Gln	Val	Asn 980	Ser	Leu	Gln	Thr	Val 985	Cys	Thr	Asn	Ile	Tyr 990	Lys	Ile
Leu	Leu	Leu 995	Gln	Ala	Tyr		Phe 000	His	Ala	Cys		Leu 005	Gln	Leu	Pro

Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile 1010 1015 1020

Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala

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1025
                    1030
                                        1035
                                                            1040
 Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly
                1045
                                    1050
 Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
                                1065
 Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
 <210> 51
 <211> 2135
 <212> DNA
 <213> Homo sapiens
<220>
<221> modified base
<222> (1871)..(1873)
<223> Wherein N is A, C, G or T
<220>
<223> N-Terminal Truncated Telomerase (ver. 2); with
      Intron Y
<400> 51
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gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
gacgcacgge egececege egececetec tteegecagg tgggeeteee eggggtegge 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gegectacea ggtgtgeggg cegeeggtgt accagetegg cgctgecact caggeegge 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
geoecceate cacategegg ceaccaegte cetgggacae geettgteee eeggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagete tetgaggece ageetgaetg gegeteggag getegtggag accatettte 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560
getteeteag gaacaceaag aagtteatet eeetggggaa geatgeeaag etetegetge 1620
aggagetgae gtggaagatg agegtgeggg aetgegettg getgegeagg ageceagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
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ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
 gcattggaat nnngacagtc accagggggg ttgaccgccg gactgggcgt ccccagggtt 1920
 gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggcgtctggc 1980
 tggcatgggt ggacgtggcc ccgggcatgg ccttctgcgt gtgctgccgt gggtgccctg 2040
 agccctcact gagtcggtgg gggcttgtgg cttcccgtga gcttccccct agtctgttgt 2100
 ctggctgagc aagcctcctg aggggctctc tattg
 <210> 52
 <211> 622
 <212> PRT
 <213> Homo sapiens
 <220>
 <223> N-Terminal Truncated Telomerase (ver.2); encoded
       by SEQ ID NO:51 and ORF1 of Intron Y
 <400> 52
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
              20
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
                                 105
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
                            120
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
                        135
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
                    150
                                         155
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
                165
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
                                185
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro
        195
                            200
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
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	210)				215)				220)			
Ser 225	Gly	Pro	Arg	g Arg	230	g Leu)	Gly	Cys	: Glu	235		Trp	Asr	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Let 250	ı Pro	Ala	Pro	Gly	Ala 255	Arg
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	ı Pro	Leu	Pro	Lys 270		Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	, Thr	Pro	Val 285		Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315		Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Àla	Ala	Val	Thr	Pro 455	Ala	Äla	Gly	Val	Cys 460	Ala	Arg	[·] Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu		Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Slv :	Ser :	Ara	His	Asn	Glu	Δra	Δra	Dho	T OU	7~~	7 an	mh w	т	T	DI-

515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 535 540

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545 550 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 570 575

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 585 590

Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly 610 615 620

<210> 53

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<223> Splicing Variant of Human Telomerase encoded by
 Intron Y, ORF2, berfore the termination codon.
 SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this
 fragment

<400> 53

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 1 5 10

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala 65 70 75 80

Ser Gly Trp Gly

<210> 54

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<223> N-Terminal Truncated Telomerase (ver. 2); encoded
by SEQ ID NO:51, with Y intron, ORF2, after the
termination codon

<400> 54

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser $165 \\ 170 \\ 175$

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro 195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro 245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu 275 280 285

Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr 290 295 300

Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 305 310 315 320

Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 325 330 335

Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys 340 345 350

Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 355 360 365

Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val 370 375 380

Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 385 390 395 400

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys
435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 450 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly 530 535

<210> 55

<211> 2145

<212> DNA

<213> Homo sapiens

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<220>
 <223> Truncated Protein 1 (ver.2); with Introns Y and 1
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 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120
 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180
 gacgcacggc cgcccccgc cgcccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360
agaggctgtg cgagcgcgc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
geoecccate cacategegg ceaccaegte eetgggacae geettgteee eeggtgtacg 1080
ccgagaccaa gcacttcctc tactcctcag gcgacaagga gcagctgcgg ccctccttcc 1140
tactcagete tetgaggeee ageetgactg gegeteggag getegtggag accatettte 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
actggcaaat gcggccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320
gggtgctcct caagacgcac tgcccgctgc gagctgcggt caccccagca gccggtgtct 1380
gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440
gtcgcctggt gcagctgctc cgccagcaca gcagccctg gcaggtgtac ggcttcgtgc 1500
gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttcctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgctgc 1620
aggagetgae gtggaagatg agegtgeggg actgegettg getgegeagg ageceagggg 1680
ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800
ccacgtttca aaagaacagg ctcttttct accggaagag tgtctggagc aagttgcaaa 1860
gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980
ageetgaegg getgeggeeg attgtgaaea tggaetaegt egtgggagee agaaegttee 2040
gcagagaaaa gagggtggct gtgctttggt ttaacttcct ttttaaccag aagccgagcg 2100
teteaceteg agggtgaagg caetgtteag egtgeteaae taega
<210> 56
<211> 704
<212> PRT
<213> Homo sapiens
<220>
<223> Truncated Protein 1 (ver.2); encoded by SEQ ID
      NO:55, with Y Intron ORF1
<400> 56
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
                                                         15
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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- Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45
- Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60
- Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 65 70 75 80
- Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu 85 90 95
- Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys 100 105 110
- Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 115 120 125
- Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140
- Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160
- Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 165 170 175
- Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 190
- Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205
- Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220
- Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240
- Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255
- Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265 270
- Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 275 280 285
- Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300
- Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 305 310 315 320
- Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 325 330 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 405 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 435 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 505 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 535 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 570 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 600 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 630 635

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu 675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly 690 695 700

<210> 57

<211> 619

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2): encoded by SEQ ID
 NO:55, with Intron Y ORF2 after the termination
 codon

<400> 57

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

Val Leu Gl
n Arg Leu Cys Glu Arg Gly Ala Lys As
n Val Leu Ala Phe35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser 170 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 185 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 215 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 235 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro 265 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu 280 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr 295 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp 310 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 325 330 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 355 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 395 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 425 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg 530 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 580 590

Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu 595 600 605

Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly 610 615

<210> 58

<211> 704

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID NO:55, with Intron Y ORF3

<400> 58

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 1 5 10 15

His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg 65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu

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Glı	n Ar	g Aro	g Arg	g Lei	ı Arç	g Ala	a Leu	1 Pro	Pro	o Glr	n Val	l Sei	Cys 110		ı Ly
Glu	ı Leı	ı Val	l Ala	a Arg	g Val	L Le	ا Glr 120	Arg	y Lei	ı Cys	s Glu	ı Arç 125		/ Ala	a Ly
Asr	n Val 130	L Let	ı Ala	a Phe	e Gly	Phe 135	e Ala	Let	ı Leu	ı Asp	Gl <u>y</u> 140		a Arç	g Gly	/ Gl
Pro 145	Pro	Glı	ı Ala	Phe	Thr 150	Thi	s Ser	Val	. Arg	y Ser 155	Туг	Leu	ı Pro	Asr	Th:
Val	. Thr	: Asp	Ala	Leu 165	Arg	g Gly	/ Ser	Gly	Ala 170	Trp	Gly	/ Leu	l Leu	Leu 175	
Arg	r Val	Gly	Asp 180	Asp	Val	Leu	ı Val	His 185		Leu	Ala	a Arg	Cys 190		Leu
Phe	Val	Leu 195	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205		Pro	Pro
Leu	Tyr 210	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220		Pro	His	Ala
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	
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Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Glỳ 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu

Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu

38	5				390)				39	5				400
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Pro	o Glr	n Ar	g Ty:	r Trp O	o Glr	n Met	t Ar	g Pro 42	o Lei	u Ph	e Le	u Gl	u Le		u Gly
Asr	n His	3 Ala 43	a Gli 5	n Cys	s Pro	Туі	Gly 440	y Val	Lei	u Le	u Ly	s Thi		s Cy:	s Pro
Leu	450	g Ala	a Ala	a Val	. Thr	Pro 455	Ala	a Ala	a Gly	y Val	1 Cys 460		a Ar	g Glı	ı Lys
Pro 465	Glr	n Gly	/ Sei	r Val	Ala 470	Ala	Pro	Glı	ı Glu	a Glu 475		Thi	Asp	Pro	Arg 480
Arg	leu	ı Val	. Glr	1 Leu 485	Leu	Arç	g Glr	His	Ser 490		Pro	Trp	Glr	val 495	
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Gly	Ser	Arg 515	His	: Asn	Glu	Arg	Arg 520	Phe	Leu	ı Arg	, Asn	Thr 525		Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540		Leu	Thr	Trp
Lys 545	Met	Ser	Val	Arg	Asp 550	Cys	Ala	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560
Gly	Cys	Val	Pro	Ala 565	Ala	Glu	His	Arg	Leu 570	Arg	Glu	Glu	Ile	Leu 575	Ala
Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu 590	Leu	Arg
Ser	Phe	Phe 595	Tyr	Val	Thr	Glu	Thr 600	Thr	Phe	Gln	Lys	Asn 605	Arg	Leu	Phe
Phe	Tyr 610	Arg	Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620	Ile	Gly	Ile	Arg
Gln 625	His	Leu	Ĺys	Arg	Val 630	Gln	Leu	Arg	Glu	Leu 635	Ser	Glu	Ala	Glu	Val 640
Arg	Gln	His	Arg	Glu 645	Ala	Arg	Pro	Ala	Leu 650	Leu	Thr	Ser	Arg	Leu 655	Arg
Phe	Ile	Pro	Lys 660	Pro	Asp	Gly	Leu	Arg 665	Pro	Ile	Val	Asn	Met 670	Asp	Tyr
Val	Val	Gly 675	Ala	Arg	Thr	Phe	Arg 680	Arg	Glu	Lys	Arg	Val 685	Ala	Val	Leu
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690 695 700

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 <213> Homo sapiens
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cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgcctgg 180
gacgcacggc cgcccccgc cgcccctcc ttccgccagg tgggcctccc cggggtcggc 240
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tecacaggge etggegeace ttegtgetge gtgtgeggge ecaggaeeeg eegeetgage 2220
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cggaggtcat cgccagcatc atcaaacccc agaacacgta ctgcgtgcgt cggtatgccg 2340
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cagtgccagg ggatcccgca gggctccatc ctctccacgc tgctctgcag cctgtgctac 2460
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<210> 60

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:59, with Intron Y ORF1

<400> 60

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg
165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220

Ser 225	Gly	y Pro	o Ar	g Ar	g Arg 230	g Lei	ı Gly	у Суз	s Gl	u Aro 23	g Ala 5	a Trp	Ası	n His	Ser 240
Val	Arg	g Glu	ı Ala	a Gly 245	y Val	L Pro) Lei	ı Gly	y Lei 25		o Ala	a Pro	o Gly	y Ala 255	
Arg	y Arg	g Gly	7 Gly 260	y Sei	c Ala	a Ser	a Arg	g Sei 265	Lei	u Pro) Let	ı Pro	270		g Pro
Arg	, Arg	g Gly 275	/ Ala	a Alá	a Pro	Glu	280	Glu	ı Arç	g Thi	r Pro	Val 285		/ Glr	n Gly
Ser	Trp 290	Alá	His	s Pro	Gly	295	Thr	Arç	g Gly	y Pro	Ser 300		Arç	g Gly	Phe
Cys 305	Val	. Val	Ser	Pro	310	Arg	Pro	Ala	Gli	315	ı Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330) Ser	Val	Gly	Arg 335	
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	g Pro	Pro	Arg	Pro 350		Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365		Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380		Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys 760 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro 795

Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln

Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala 820 825 830

Gly Arg Ala Ala Pro Ala Phe Val Gly 835 840

<210> 61

<211> 756

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:59 with Intron Y ORF2 after the termination codon

<400> 61

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg
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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 145 . 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro 195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 210 215 220

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Th	r Ar	g Hi	s Se	r His 24	s Pro	o Sei	r Va.	l Gl	y Ar 25	g Gli 0	n Hi:	s Hi	s Al	a Gl 25	y Pro 5
Pro	Se:	r Th	r Se: 26	r Arg	g Pro) Pro	Ar	g Pro 26!	o Tr _j 5	p Asp	o Thi	r Pro	o Cy:		o Pro
Va:	l Туі	r Ala 27	a Glu 5	ı Thi	r Lys	s His	Phe 280	e Lei	а Ту	r Sei	s Sei	Gl ₂		o Lys	s Glu
Glr	1 Let 290	ı Arç	g Pro	Ser	: Ph∈	295	ı Leı	ı Sei	Sei	r Leu	a Arç 300		Sei	. Lei	ı Thr
Gl ₃ 305	Ala	a Arg	g Arc	g Leu	1 Val 310	Glu	Thr	: Ile	e Phe	e Leu 315	ı Gly	/ Ser	Arg	g Pro	Trp 320
Met	Pro	Gly	7 Thr	Pro 325	Arg	Arg	Leu	Pro	330	g Leu)	Pro	Glr	Arg	Tyr 335	Trp
Gln	Met	: Arg	340	Leu	Phe	Leu	Glu	Leu 345	Leu	ı Gly	Asn	His	350		Cys
Pro	Tyr	Gly 355	Val	Leu	Leu	Lys	Thr 360	His	Cys	Pro	Leu	Arg 365	Ala	Ala	Val
Thr	Pro 370	Ala	Ala	Gly	Val	Cys 375	Ala	Arg	Glu	Lys	Pro 380	Gln	Gly	Ser	Val
Ala 385	Ala	Pro	Glu	Glu	Glu 390	Asp	Thr	Asp	Pro	Arg 395	Arg	Leu	Val	Gln	Leu 400
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Cys	Leu	Arg	Arg 420	Leu	Val	Pro	Pro	Gly 425	Leu	Trp	Gly	Ser	Arg 430	His	Asn
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His	Ala 450	Lys	Leu	Ser	Leu	Gln 455	Glu	Leu	Thr	Trp	Lys 460	Met	Ser	Val	Arg
Asp 465	Cys	Ala	Trp	Leu	Arg 470	Arg	Ser	Pro	Gly	Val 475	Gly	Cys	Val	Pro	Ala 480
Ala	Glu	His	Arg	Leu 485	Arg	Glu	Glu	Ile	Leu 490	Ala	Lys	Phe	Leu	His 495	Trp
Leu	Met	Ser	Val 500	Tyr	Val	Val	Glu	Leu 505	Leu	Arg	Ser	Phe	Phe 510	Tyr	Val
Thr	Glu	Thr 515	Thr	Phe	Gln	Lys	Asn 520	Arg	Leu	Phe	Phe	Tyr 525	Arg	Lys	Ser

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg 530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 580 585 590

Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys 595 600 605

Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu 610 615 620

Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 625 630 635 635

Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr 645 650 655

Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp 660 665 670

Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr 675 680 685

Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val 690 695 700

Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro 705 710 715 720

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg 725 730 735

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro 740 745 750

Ala Phe Val Gly 755

<210> 62

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:
59 with Intron Y ORF3

<400> 62

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Ala	a Lei 5	u Va)	l Ala	a Gln	n Cys	Leu 55	Val	. Cys	s Val	l Pro	Trp 60		o Ala	a Ar	g Pro
Pro 65	Pro	o Al	a Ala	Pro	Ser 70	Phe	Arg	g Glr	n Val	Pro 75		Arç	g Gly	y Aro	g Arc 80
Pro	Alá	a Gl	y Val	Glu 85	Gly	Gly	Arg	Gly	7 Glu 90	ı Pro) Ala	Thi	c Cys	Gl _y 95	
Glr	n Arç	y Ar	g Arg 100	Leu	Arg	Ala	Leu	Pro 105	Pro	Glr	n Val	Ser	Cys		Lys
Glu	ı Lev	115	l Ala	Arg	Val	Leu	Gln 120	Arg	Leu	Суѕ	Glu	Arg 125		'Ala	Lys
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Phe	Val	Leu 195	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205	Gly	Pro	Pro
Leu	Tyr 210	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Glỳ	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly i	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys	Val	Val	Ser	Pro .	Ala A	Arg	Pro .	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu

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His	s Hi	s Al	a Gl 34	y Pro	o Pro	Se:	r Thi	s Sei 34!	r Arg	g Pro	o Pro	Arç	g Pro 350		Asp
Thi	r Pro	Cy 35	s Pro 5	o Pro	o Val	L Туі	Ala 360	a Glu	ı Thi	r Lys	s His	Phe 365	e Leu	туг	Ser
Ser	Gly 370	y Asj	p Ly:	s Glu	ı Glr	1 Let 375	ı Arç	g Pro	Sei	c Ph∈	280		ı Ser	Ser	Leu
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Leu	Arg 450	Ala	a Ala	ı Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	ser Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys 545	Меt	Ser	Val	Arg	Asp 550	Cys	Àla	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560
Gly	Cys	Val	Pro	Ala 565	Ala	Glu	His	Arg	Leu 570	Arg	Glu	Glu	Ile	Leu 575	Ala
Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu 590	Leu	Arg
Ser	Phe	Phe 595	Tyr	Val	Thr	Glu	Thr 600	Thr	Phe	Gln		Asn 605	Arg	Leu	Phe
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Ara

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Gln 625	His	s Lei	u Lys	s Arg	y Val 630	. Gln	Let	ı Arç	g Glu	Let 635	ı Sei	r Glı	ı Ala	a Glu	ا Val 640	
Arg	Glr	n His	s Arg	Glu 645	ı Ala	Arg	Pro	Ala	Leu 650	Lei	ı Thr	Sei	a Arg	J Let 655	ı Arg	
Phe	Ile	e Pro	660	Pro	Asp	Gly	Leu	Arg 665	Pro	Ile	e Val	Asr	Met 670		Tyr	
Val	Val	Gly 675	Ala	Arg	Thr	Phe	Arg 680	Arg	Glu	Lys	Arg	Ala 685		Arg	, Leu	
Thr	Ser 690	Arg	, Val	Lys	Ala	Leu 695	Phe	Ser	Val	Leu	Asn 700	Tyr	Glu	Arg	Ala	
Arg 705	Arg	Pro	Gly	Leu	Leu 710	Gly	Ala	Ser	Val	Leu 715	Gly	Leu	Asp	Asp	Ile 720	
			Trp	125					730					735		
			Leu 740					/45					750			
		,55	Gln				760					765				
	, , ,		Thr			115					780					
,00			His		790					795					800	
			Asp	005					810					815		
Pro	Val	Leu	Arg 820	Arg	His	Gly	Glu	Gln 825	Ala	Val	Cys	Gly	Asp 830	Ser	Ala	
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<223> Reference Protein (ver.2); with Introns Y, Alpha

and Beta

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greeggerg	y ggilgagggo	c ggccggggg	j aaccagegad	c atacaaaaa	a cadedeada	~ 300
gactcaggg	gcttccccc	g caggtgtcct	gcctgaagga	actaataac	Casatacta	360
agaggctgt	g cgagcgcgg	c gcgaagaacg	r ťactaaccťt	caacttcac	r ctactaasc	120
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cggtgaccga	a cacactaca	g gggagcgggg	r catagaaact	: gegeageeac	cogcicaaca	40U
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gcgcctacca	agtatacaa	r ccaccactat	: gogogotocc	. cgcyccygc	geteecaget	600
ccccacaca	a cactaataa	g ccgccgctgt	accagerege	g cyclyceaet	caggcccggc	660
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acaataccaa	r ccassatata	cccctgggcc	tgccagecec	gggtgcgagg	g aggcgcgggg	j 780
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cccccgagge	cgtgcagtgg	ctgtgccacc	aagcattcct	gctcaagctg	actigacacc	3360
gryrcaccia	egigecacie	ctggggtcac	tcaggacagc	ccadacdcad	ctgagtcgga	3420
ayereeeggg	gacgacgctg	actgccctgg	aggeegeage	caacccddda	ctacceteaa	3480
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<211> 1165

<212> PRT

<213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF1

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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220

Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

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Ser	Trp 290	Ala	a His	Pro	Gly	/ Arc 295		Arg	Gly	Pro	Ser 300		Arg	Gly	Phe
Cys 305	Val	. Val	l Ser	Pro	310	Arg	g Pro	Ala	Glu	315		Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	ı Ser	Gly 325	Thr	Arg	, His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345		Pro	Pro	Arg	Pro 350		Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	Hìs	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val

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Gly	v Cys	s Val	l Pro	Ala 565	Ala	Glu	His	Arg	Leu 570		g Glı	ı Glı	ı Ile	E Leu 575	ı Ala
Lys	Phe	e Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	. Val	. Val	. Glu	1 Let 590		a Arg
Ser	Phe	Phe 595	e Tyr	· Val	Thr	Glu	Thr 600	Thr	Phe	e Gln	Lys	Asr 605		, Leu	Phe
Phe	Tyr 610	Arg	Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620		e Gly	'Ile	Arg
Gln 625	His	Leu	Lys	Arg	Val 630	Gln	Leu	Arg	Glu	Leu 635		Glu	Ala	Glu	Val 640
Arg	Gln	His	Arg	Glu 645	Ala	Arg	Pro	Ala	Leu 650	Leu	Thr	Ser	Arg	Leu 655	Arg
Phe	Ile	Pro	Lys 660	Pro	Asp	Gly	Leu	Arg 665	Pro	Ile	Val	Asn	Met 670	Asp	Tyr
Val	Val	Gly 675	Ala	Arg	Thr	Phe	Arg 680	Arg	Glu	Lys	Arg	Ala 685		Arg	Leu
Thr	Ser 690	Arg	Val	Lys	Ala	Leu 695	Phe	Ser	Val	Leu	Asn 700	Tyr	Glu	Arg	Ala
Arg 705	Arg	Pro	Gly	Leu	Leu 710	Gly	Ala	Ser	Val	Leu 715	Gly	Leu	Asp	Asp	Ile 720
His	Arg	Ala	Trp	Arg 725	Thr	Phe	Val	Leu	Arg 730	Val	Arg	Ala	Gln	Asp 735	Pro
Pro	Pro	Glu	Leu 740	Tyr	Phe	Val	Lys	Val 745	Asp	Val	Thr	Gly	Ala 750	Tyr	Asp
Thr	Ile	Pro 755	Gln	Asp	Arg	Leu	Thr 760	Glu	Val	Ile	Ala	Ser 765	Ile	Ile	Lys
Pro	Gln 770	Asn	Thr	Tyr	Cys	Val 775	Arg	Arg	Tyr	Ala	Val 780	Val	Gln	Lys	Ala
Ala [.] 785	His	Gly	His	Val	Arg 790	Lys	Ala	Phe	Lys	Ser 795	His	Val	Ser	Thr	Leu 800
Thr	Asp	Leu	Gln	Pro 805	Tyr	Met	Arg	Gln	Phe 810	Val	Ala	His	Leu	Gln 815	Glu
Thr	Ser	Pro	Leu 820	Arg	Asp .	Ala	Val	Val 825	Ile	Glu	Gln	Ser	Ser 830	Ser	Leu
Asn	Glu	Ala 835	Ser	Ser	Gly	Leu	Phe 840	Asp	Val	Phe		Arg 845	Phe	Met	Cys
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Gly	Asp) Met	: Glu	885	Lys	Leu	Phe	Ala	a Gly 890		Arg	Arg	Asp	Gly 895	
Leu	. Leu	Arg	900	val	Asp	Asp	Phe	Leu 905	Leu i	Val	Thr	Pro	His 910	Leu	Th.
His	Ala	Lys 915	Thr	Phe	Leu	Arg	Thr 920	Leu	ı Val	Arg	Gly	Val 925		Glu	Ту
Gly	Cys 930	Val	Val	Asn	Leu	Arg 935	Lys	Thr	Val	Val	Asn 940		Pro	Val	Glı
Asp 945	Glu	Ala	Leu	Gly	Gly 950	Thr	Ala	Phe	Val	Gln 955	Met	Pro	Ala	His	Gl ₂ 960
Leu	Phe	Pro	Trp	Cys 965	Gly	Leu	Leu	Leu	Asp 970	Thr	Arg	Thr	Leu	Glu 975	Val
Gln	Ser	Asp	Tyr 980	Ser	Ser	Tyr	Ala	Arg 985	Thr	Ser	Ile	Arg	Ala 990	Ser	Let
Thr	Phe	Asn 995	Arg	Gly	Phe	Lys	Ala 1000	Gly	Arg	Asn		Arg 1005	Arg	Lys	Leu
Phe	Gly 1010	Val	Leu	Arg	Leu	Lys 1015	Cys	His	Ser		Phe 1020	Leu	Asp	Leu	Glr
Val 102	Asn 5	Ser	Leu	Gln	Thr 1030	Val	Cys	Thr	Asn	Ile 1035	Tyr	Lys	Ile		Leu L040
Leu	Gln	Ala	Tyr	Arg 1045	Phe	His	Ala	Cys	Val 1050	Leu	Gln	Leu		Phe 055	His
Gln	Gln	Val	Trp 1060	Lys	Asn	Pro	Thr 1	Phe .065	Phe	Leu	Arg		Ile .070	Ser	Asp
Thr	Ser 1	Leu 1075	Cys	Tyr	Ser	Ile 1	Leu .080	Lys	Ala	Lys	Asn 1	Ala .085	Gly	Met	Ser
Leu 1	Gly .090	Ala	Lys	Gly	Ala 1	Ala .095	Gly	Pro	Leu		Ser 100	Glu	Ala	Val	Gln
Trp 1105	Leu	Cys	His	Gln 1	Ala 110	Phe	Leu	Leu	Lys 1	Leu 115	Thr	Arg	His	Arg 1	Val 120
Thr	Tyr	Val	Pro 1	Leu 125	Leu	Gly	Ser	Leu 1	Arg 130	Thr	Ala	Gln		Gln 135	Leu
Ser	Arg	Lys 1	Leu 140	Pro	Gly	Thr	Thr 1	Leu 145	Thr	Ala	Leu	Glu 1	Ala . 150	Ala	Ala
Asn	Pro	Ala	Leu	Pro	Ser	Asp	Phe	Lys	Thr	Ile	Leu	Asp			

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1165

<210> 65

<211> 1081

<212> PRT

<213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63 with Intron Y ORF2 after the termination codon

<400> 65

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly 115

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 135

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 155

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala 185

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly 225 235

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr 295 300 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp 325 Gln Met Arg Pro Leu Phe Leu Glu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val 355 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 385 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 420 425 430

Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 435 440 445

His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg 530 535 540

Val 545	Glr	ı Lev	a Arg	g Glu	Leu 550	Ser	Glu	Ala	Glu	Val 555		g Glr	n His	Arg	Glu 560
Ala	Arç	g Pro	Ala	Leu 565	Leu	Thr	Ser	Arg	Leu 570		g Phe	: Ile	e Pro	Lys 575	Pro
Asp	Gly	/ Let	Arg 580	Pro	Ile	Val	. Asn	Met 585	Asp	Tyr	. Val	Val	. Gly 590		Arg
Thr	Phe	Arg 595	Arg	Glu	Lys	Arg	Ala 600		Arg	Leu	Thr	Ser 605		Val	Lys
Ala	Leu 610	Phe	Ser	Val	Leu	Asn 615	Tyr	Glu	Arg	Ala	Arg 620		Pro	Gly	Leu
Leu 625	Gly	Ala	Ser	Val	Leu 630	Gly	Leu	Asp	Asp	Ile 635	His	Arg	Ala	Trp	Arg 640
Thr	Phe	Val	Leu	Arg 645	Val	Arg	Ala	Gln	Asp 650	Pro	Pro	Pro	Glu	Leu 655	_
Phe	Val	Lys	Val 660	Asp	Val	Thr	Gly	Ala 665	Tyr	Asp	Thr	Ile	Pro 670	Gln	Asp
Arg	Leu	Thr 675	Glu	Val	Ile	Ala	Ser 680	Ile	Ile	Lys	Pro	Gln 685	Asn	Thr	Tyr
Cys	Val 690	Arg	Arg	Tyr	Ala	Val 695	Val	Gln	Lys	Ala	Ala 700	His	Gly	His	Val
Arg 705	Lys	Ala	Phe	Lys	Ser 710	His	Val	Ser	Thr	Leu 715	Thr	Asp	Leu	Gln	Pro 720
Tyr	Met	Arg	Gln	Phe 725	Val	Ala	His	Leu	Gln 730	Glu	Thr	Ser	Pro	Leu 735	Arg
Asp	Ala	Val	Val 740	Ile	Glu	Gln	Ser	Ser 745	Ser	Leu	Asn	Glu	Ala 750	Ser	Ser
Gly	Leu	Phe 755	Asp	Val	Phe	Leu	Arg 760	Phe	Met	Cys	His	His 765	Ala	Val	Arg
Ile	Arg 770	Gly	Lys	Ser	Tyr	Val 775	Gln	Cys	Gln	Gly	Ile 780	Pro	Gln	Gly	Ser
Ile 785	Leu	Ser	Thr	Leu	Leu 790	Cys	Ser	Leu	Cys	Tyr 795	Gly	Asp	Met	Glu	Asn 800
Lys	Leu	Phe	Ala	Gly 805	Ile	Arg	Arg	Asp	Gly 810	Leu	Leu	Leu	Arg	Leu 815	Val
Asp	Asp	Phe	Leu 820	Leu	Val	Thr	Pro	His 825	Leu	Thr	His	Ala	Lys 830	Thr	Phe
Leu	Arg	Thr 835	Leu	Val	Arg		Val 840	Pro	Glu	Tyr		Cys 845	Val	Val	Asn

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly 850 855 860

Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys 865 870 875 880

Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser 885 890 895

Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly 900 905 910

Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg 915 920 925

Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln 930 935 940

Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln Ala Tyr Arg 945 950 955 960

Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys 965 970 975

Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys 980 985 990

Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys 995 1000 1005

Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His 1010 1015 1020

Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro 1025 1030 1035 1040

Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu 1045 1050 1055

Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu 1060 1065 1070

Pro Ser Asp Phe Lys Thr Ile Leu Asp 1075

<210> 66

<211> 1165

<212> PRT

<213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63
 with Intron Y ORF3

<400> 66

- Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$
- His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30
- Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45
- Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60
- Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg 65 70 75 80
- Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu 85 90 95
- Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
 115 120 125
- Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140
- Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160
- Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg 165 170 175
- Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 190
- Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205
- Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220
- Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240
- Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg
 245 250 255
- Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 260 265 270
- Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 275 280 285
- Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295 300

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 310 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 380 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 425 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg 465 475 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 505 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 535 540 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 570 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 600

Ph	е Ту 61	r Ar O	g Ly	s Se	r Val	1 Trp 615	Sei	c Lys	s Lei	ı Glr	Ser 620		e Gly	/ Ile	e Arg
Gl: 62	n Hi: 5	s Le	u Ly	s Ar	g Val 630	l Glr	ı Lei	ı Arç	g Glu	Leu 635	ser	Glu	ı Ala	a Glu	Val 640
Ar	g Gli	n Hi	s Ar	g Gli 645	ı Ala	a Arç	J Pro	Ala	Leu 650	ı Lev	Thr	Ser	Arç	655	Arg
Phe	e Ile	e Pro	0 Ly:	s Pro	Asp	Gly	Leu	Arç 665) Ile	· Val	Asn	Met 670		Tyr
Va]	l Val	67	y Ala 5	a Arg	g Thr	Phe	Arg 680	Arg	Glυ	Lys	Arg	Ala 685		Arg	Leu
Thr	Ser 690	Arq	g Val	Lys	a Ala	Leu 695	Phe	Ser	Val	. Leu	Asn 700	Tyr	Glu	Arg	Ala
Arç 705	Arç	g Pro	Gl)	Leu	Leu 710	Gly	Ala	Ser	Val	Leu 715	Gly	Leu	Asp	Asp	Ile 720
His	Arg	, Ala	Trp	725	Thr	Phe	Val	Leu	Arg 730	Val	Arg	Ala	Gln	Asp 735	Pro
Pro	Pro	Glu	740	Tyr	Phe	Val	Lys	Val 745	Asp	Val	Thr	Gly	Ala 750	Tyr	Asp
Thr	Ile	Pro 755	Gln	Asp	Arg	Leu	Thr 760	Glu	Val	Ile	Ala	Ser 765	Ile	Ile	Lys
Pro	Gln 770	Asn	Thr	Tyr	Cys	Val 775	Arg	Arg	Tyr	Ala	Val 780	Val	Gln	Lys	Ala
Ala 785	His	Gly	His	Val	Arg 790	Lys	Ala	Phe	Lys	Ser 795	His	Val	Ser	Thr	Leu 800
Thr	Asp	Leu	Gln	Pro 805	Tyŗ	Met	Arg	Gln	Phe 810	Val	Ala	His	Leu	Gln 815	Glu
Thr	Ser	Pro	Leu 820	Arg	Asp	Ala	Val	Val 825	Ile	Glu	Gln	Ser	Ser 830	Ser	Leu
Asn	Glu	Ala 835	Ser	Ser	Gly	Leu	Phe 840	Asp	Val	Phe	Leu	Arg 845	Phe	Met	Cys
His	His 850	Ala	Val	Arg	Ile	Arg 855	Gly	Lys	Ser	Tyr	Val 860	Gln	Cys	Gln	Gly
Ile 865	Pro	Gln	Gly	Ser	Ile 870	Leu	Ser	Thr	Leu	Leu 875	Cys	Ser	Leu	Cys	Tyr 880
Gly	Asp	Met	Glu	Asn 885	Lys	Leu	Phe	Ala	Gly 890	Ile	Arg	Arg	Asp	Gly 895	Leu
Leu	Leu	Arg	Leu 900	Val	Asp	Asp	Phe	Leu 905	Leu	Val	Thr		His 910	Leu	Thr

- His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 915 920 925
- Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu 930 935 940
- Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly 945 950 955 960
- Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 965 970 975
- Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu 980 985 990
- Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu 995 1000 1005
- Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln 1010 1015 1020
- Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 1025 1030 1035 1040
- Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His 1045 1050 1055
- Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp 1060 1065 1070
- Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser 1075 1080 1085
- Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln 1090 1095 1100
- Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val 1105 1110 1115 1120
- Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu 1125 1130 1135
- Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala 1140 1145 1150
- Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1155 1160 1165
- <210> 67
- <211> 3173
- <212> DNA
- <213> Homo sapiens
- <220>
- <223> Truncated Protein (ver.2); with Introns Y, Alpha, Beta and 2

<400> 67 atgeegegeg eteceegetg eegageegtg egeteeetge tgegeageea etacegegag 60 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180 gacgcaegge egececege egececetee tteegecagg tgggeeteee eggggtegge 240 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgctgc 360 agaggetgtg egagegegge gegaagaaeg tgetggeett eggettegeg etgetggaeg 420 gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600 gegeetacea ggtgtgeggg cegeegetgt accagetegg egetgeeact caggeegge 660 eccegecaca egetagtgga eccegaagge gtetgggatg egaacgggee tggaaccata 720 gegtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780 geagtgeeag ecgaagtetg cegttgeeca agaggeecag gegtggeget geecetgage 840 cggageggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900 gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960 agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020 geoceccate cacategegg ceaccaegte cetgggacae geettgteee eeggtgtacg 1080 cogagaceaa geaetteete taeteeteag gegaeaagga geagetgegg ceeteettee 1140 tactcagete tetgaggeee ageetgactg gegeteggag getegtggag accatettte 1200 tgggttecag geeetggatg ceagggaete eeegcaggtt geeegeetg eeecageget 1260 actggcaaat gcggcccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320 gggtgeteet caagacgeae tgeeegetge gagetgeggt caceccagea geeggtgtet 1380 gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440 gtcgcctggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500 gggcctgcct gcgccggctg gtgcccccag gcctctgggg ctccaggcac aacgaacgcc 1560. getteeteag gaacaccaag aagtteatet eeetggggaa geatgeeaag etetegetge 1620 aggagetgae gtggaagatg agegtgeggg aetgegettg getgegeagg ageeeagggg 1680 ttggctgtgt tccggccgca gagcaccgtc tgcgtgagga gatcctggcc aagttcctgc 1740 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttctttat gtcacggaga 1800 ccacgtttca aaagaacagg ctcttttct accggaagag tgtctggagc aagttgcaaa 1860 gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920 tcaggcagca tcgggaagcc aggcccgccc tgctgacgtc cagactccgc ttcatcccca 1980 agectgacgg getgeggeeg attgtgaaca tggactacgt egtgggagee agaacgttee 2040 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100 actacgageg ggegegege eeeggeetee tgggegeete tgtgetggge etggaegata 2160 tecacaggge etggegeace ttegtgetge gtgtgeggge ecaggaeceg eegeetgage 2220 tgtactttgt caaggtggat gtgacgggcg cgtacgacac catececcag gacaggetca 2280 eggaggteat egecageate ateaaacee agaacaegta etgegtgegt eggtatgeeg 2340 tggtccagaa ggccgcccat gggcacgtcc gcaaggcctt caagagccac gtctctacct 2400 tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag accagcccgc 2460 tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520 togacgtett cetacgette atgtgceaec acgeegtgeg cateagggge aagteetaeg 2580 tocagigoca ggggatocog cagggotoca toctotocac gotgototgc agootgtgct 2640 acggcgacat ggagaacaag ctgtttgcgg ggattcggcg ggacgggctg ctcctgcgtt 2700 tggtggatga tttcttgttg gtgacacete aceteaceca egegaaaace ttcctcagga 2760 ccctggtccg aggtgtccct gagtatggct gcgtggtgaa cttgcggaag acagtggtga 2820 acttccctgt agaagacgag gccctgggtg gcacggcttt tgttcagatg ccggcccacg 2880 gectattece etggtgegge etgetgetgg ataceeggae eetggaggtg eagagegaet 2940 actocaggtg agegeacetg geoggaagtg gageetgtge eeggetgggg eaggtgetge 3000 tgcagggccg ttgcgtccac ctctgcttcc gtgtggggca ggcgactgcc aatcccaaag 3060 ggtcagatgc cacagggtgc ccctcgtccc atctggggct gagcacaaat gcatctttct 3120 gtgggagtga gggtgcctca caacgggagc agttttctgt gctattttgg taa 3173

<211> 982

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (ver.2); encoded by SEQ ID NO:67 with Intron Y ORF1

<400> 68

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu 85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys 100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys 115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 $$ 150 $$ 155 $$ 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 165 170 175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185 190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 195 200 205

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 215 220

Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 225 230 235 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 245 250 255

Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys 545	Met	Ser	Val	Arg	Asp 550	Cys	Ala	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560

Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 635 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 645 650 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 665 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 680 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 695 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys 760 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu 790 795 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu 805 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu 825 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly 850 855

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr 865 870 875 880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu 930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly 945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 965 970 975

Gln Ser Asp Tyr Ser Arg 980

<210> 69

<211> 897

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (ver.2); encoded by SEQ ID NO:67 with Intron Y ORF2 after the termination codon

<400> 69

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe 35 . 40 . 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro	Ser	Cys 115		Tyr	Gln	Val	Cys 120	Gly	Pro	Pro	Leu	Tyr 125	Gln	Leu	Gly
Ala	Ala 130		Gln	Ala	Arg	Pro 135	Pro	Pro	His	Ala	Ser 140	Gly	Pro	Arg	Arg
Arg 145	Leu	Gly	Cys	Glu	Arg 150	Ala	Trp	Asn	His	Ser 155	Val	Arg	Glu	Ala	Gly 160
Val	Pro	Leu	Gly	Leu 165	Pro	Ala	Pro	Gly	Ala 170	Arg	Arg	Arg	Gly	Gly 175	Ser
Ala	Ser	Arg	Ser 180	Leu	Pro	Leu	Pro	Lys 185	Arg	Pro	Arg	Arg	Gly 190	Ala	Ala
Pro	Glu	Pro 195	Glu	Arg	Thr	Pro	Val 200	Gly	Gln	Gly	Ser	Trp 205	Ala	His	Pro
Gly	Arg 210	Thr	Arg	Gly	Pro	Ser 215	Asp	Arg	Gly	Phe	Cys 220	Val	Val	Ser	Pro
Ala 225	Arg	Pro	Ala	Glu	Glu 230	Ala	Thr	Ser	Leu	Glu 235	Gly	Ala	Leu	Ser	Gly 240
Thr	Arg	His	Ser	His 245	Pro	Ser	Val	Gly	Arg 250	Gln	His	His	Ala	Gly 255	Pro
Pro	Ser	Thr	Ser 260	Arg	Pro	Pro	Arg	Pro 265	Trp	Asp	Thr	Pro	Cys 270	Pro	Pro
Val	Tyr	Ala 275	Glu	Thr	Lys	His	Phe 280	Leu	Tyr	Ser	Ser	Gly 285	Asp	Lys	Glu
Gln	Leu 290	Arg	Pro	Ser	Phe	Leu 295	Leu	Ser	Ser	Leu	Arg 300	Pro	Ser	Leu	Thr
Gly 305	Ala	Arg	Arg	Leu	Val 310	Glu	Thr	Ile	Phe	Leu 315	Gly	Ser	Arg	Pro	Trp 320
Met	Pro	Gly	Thr	Pro 325	Arg	Arg	Leu	Pro	Arg 330	Leu	Pro	Gln	Arg	Tyr 335	Trp
Gln	Met	Arg	Pro 340	Leu	Phe	Leu	Glu	Leu 345	Leu	Gly	Asn	His	Ala 350	Gln	Cys
Pro	Tyr	Gly 355	Val	Leu	Leu	Lys	Thr 360	His	Cys	Pro	Leu	Arg 365	Ala	Ala	Val
Thr	Pro 370	Ala	Ala	Gly	Val	Cys 375	Ala	Arg	Glu	Lys	Pro 380	Gln	Gly	Ser	Val
Ala 385	Ala	Pro	Glu	Glu	Glu 390	Asp	Thr	Asp	Pro	Arg 395	Arg	Leu	Val	Gln	Leu 400
Leu	Arg	Gln	His	Ser 405	Ser	Pro	Trp	Gln	Val 410	Tyr	Gly	Phe	Val	Arg 415	Ala

Cys	Leu	ı Arg	420	Leu	Val	Pro	Pro	Gly 425		Trp	Gly	y Ser	430		s Asr
Glu	Arg	Arg 435	Phe	Leu	Arg	Asn	Thr 440		Lys	Phe	: Ile	Ser 445	Leu S	ı Gly	/ Lys
His	Ala 450	Lys	Leu	Ser	Leu	Gln 455		Leu	Thr	Trp	Lys 460		: Ser	· Val	Arg
Asp 465	Cys	Ala	Trp	Leu	Arg 470	Arg	Ser	Pro	Gly	Val 475		Cys	: Val	Pro	Ala 480
Ala	Glu	His	Arg	Leu 485		Glu	Glu	Ile	Leu 490		Lys	Phe	e Leu	His 495	
Leu	Met	Ser	Val 500	Tyr	Val	Val	Glu	Leu 505		Arg	Ser	Phe	Phe 510		Val
Thr	Glu	Thr 515	Thr	Phe	Gln	Lys	Asn 520	Arg	Leu	Phe	Phe	Tyr 525	Arg	Lys	Ser
Val	Trp 530	Ser	Lys	Leu	Gln	Ser 535	Ile	Gly	Ile	Arg	Gln 540	His	Leu	Lys	Arg
Val 545	Gln	Leu	Arg	Glu	Leu 550	Ser	Glu	Ala	Glu	Val 555	Arg	Gln	His	Arg	Glu 560
Ala	Arg	Pro	Ala	Leu 565	Leu	Thr	Ser	Arg	Leu 570	Arg	Phe	Ile	Pro	Lys 575	
Asp	Gly	Leu	Arg 580	Pro	Ile	Val	Asn	Met 585	Asp	Tyr	Val	Val	Gly 590	Ala	Arg
Thr	Phe	Arg 595	Arg	Glu	Lys	Arg	Ala 600	Glu	Arg	Leu	Thr	Ser 605	Arg	Val	Lys
Ala	Leu 610	Phe	Ser	Val	Leu	Asn 615	Tyr	Glu	Arg	Ala	Arg 620	Arg	Pro	Gly	Leu
Leu 625	Gly	Ala	Ser	Val	Leu 630	Gly	Leu	Asp	Asp	Ile 635	His	Arg	Ala	Trp	Arg 640
Thr	Phe	Val	Leu	Arg 645	Val	Arg	Ala	Gln	Asp 650	Pro	Pro	Pro	Glu	Leu 655	Tyr
Phe	Val	Lys	Val 660	Asp	Val	Thr	Gly	Ala 665	Tyr	Asp	Thr	Ile	Pro 670	Gln	Asp
Arg	Leu	Thr 675	Glu	Val	Ile	Ala	Ser 680	Ile	Ile	Lys	Pro	Gln 685	Asn	Thr	Tyr
Cys	Val 690	Arg	Arg	Tyr	Ala	Val 695	Val	Gln	Lys	Ala	Ala 700	His	Gly	His	Val
Arg 705	Lys	Ala	Phe	Lys	Ser 710	His	Val	Ser	Thr	Leu 715	Thr	Asp	Leu	Gln	Pro 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn 785 795 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe 820 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly 855 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser 890

Arg

<210> 70

<211> 982

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 3 (Ver.2); encoded by SEQ ID NO:67 with Intron Y ORF3

<400> 70

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 25

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

	50					55					60				
Pro 65	Pro	Ala	Ala	Pro	Ser 70	Phe	Arg	Gln	Val	Pro 75	Pro	Arg	Gly	Arg	Arg 80
Pro	Ala	Gly	Val	Glu 85	Gly	Gly	Arg	Gly	Glu 90	Pro	Ala	Thr	Cys	Gly 95	Glu
Gln	Arg	Arg	Arg 100	Leu	Arg	Ala	Leu	Pro 105	Pro	Gln	Val	Ser	Cys 110	Leu	Lys
Glu	Leu	Val 115	Ala	Arg	Val	Leu	Gln 120	Arg	Leu	Cys	Glu	Arg 125	Gly	Ala	Lys
Asn	Val 130	Leu	Ala	Phe	Gly	Phe 135	Ala	Leu	Leu	Asp	Gly 140	Ala	Arg	Gly	Gly
Pro 145	Pro	Glu	Ala	Phe	Thr 150	Thr	Ser	Val	Arg	Ser 155	Tyr	Leu	Pro	Asn	Thr 160
Val	Thr	Asp	Ala	Leu 165	Arg	Gly	Ser	Gly	Ala 170	Trp	Gly	Leu	Leu	Leu 175	Arg
Arg	Val	Gly	Asp 180	Asp	Val	Leu	Val	His 185	Leu	Leu	Ala	Arg	Cys 190	Ala	Leu
Phe	Val	Leu 195	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205	Gly	Pro	Pro
Leu	Tyr 210		Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala
Ser 225		Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	ı Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg
Arg	g Arç	g Gly	/ Gly 260	ser	Ala	Ser	Arg	Ser 265	Let	ı Pro	Leu	Pro	Lys 270	Arg	Pro
Arq	g Arg	g Gly 275	y Ala	a Ala	Prc	Glu	Pro 280	Glu	ı Arç	g Thr	Pro	Val 285	Gly	glr Glr	Gly
Sei	Trp 290	o Ala	a His	s Pro	o Gly	Arg 295	Thr	Arg	g `Gly	y Pro	Ser 300	Asp	Arg	g Gly	' Phe
Cy:		l Vai	l Sei	r Pro	310	a Arg	g Pro	Ala	a Glu	u Glu 315	ı Ala	a Thi	s Sei	c Lev	320 320
Gl	y Ala	a Le	u Sei	r Gly 32	y Thi	r Arg	g His	s Sei	r Hi:	s Pro	o Sei	r Vai	l Gly	y Arc 33	g Gln
Hi	s Hi	s Al	a Gl; 34		o Pro	s Sei	r Thi	r Se:	r Ar	g Pr	o Pro	o Ar	g Pro 350	o Trj O	o Asp
ሞኤ	r Dr	o Cv	s Pr	o Pr	o Vai	l Tv:	r Ala	a Gl	u Th	r Ly	s Hi	s Ph	e Le	и Ту	r Ser

		355					360					365			
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Суѕ	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys 545	Met	Ser	Val	Arg	Asp 550	Cys	Ala	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560
Gly	Cys	Val	Pro	Ala 565	Ala	Glu	His	Arg	Leu 570	Arg	Glu	Glu	Ile	Leu 575	Ala
Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu 590	Leu	Arg
Ser	Phe	Phe 595	Tyr	Val	Thr	Glu	Thr 600	Thr	Phe	Gln	Lys	Asn 605	Arg	Leu	Phe
Phe	Tyr 610	Arg	Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620	Ile	Gly	Ile	Arg
Gln 625	His	Leu	Lys	Arg	Val 630	Gln	Leu	Arg	Glu	Leu 635	Ser	Glu	Ala	Glu	Val 640
Arg	Gln	His	Arg	Glu 645	Ala	Arg	Pro	Ala	Leu 650	Leu	Thr	Ser	Arg	Leu 655	Arg
Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr

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Val	Val	Gly 675	Ala	Arg	Thr	Phe	Arg 680	Arg	Glu	Lys	Arg	Ala 685	Glu	Arg	Leu
Thr	Ser 690	Arg	Val	Lys	Ala	Leu 695	Phe	Ser	Val	Leu	Asn 700	Tyr	Glu	Arg	Ala
Arg 705	Arg	Pro	Gly	Leu	Leu 710	Gly	Ala	Ser	Val	Leu 715	Gly	Leu	Asp	Asp	Ile 720
His	Arg	Ala	Trp	Arg 725	Thr	Phe	Val	Leu	Arg 730	Val	Arg	Ala	Gln	Asp 735	Pro
Pro	Pro	Glu	Leu 740	Tyr	Phe	Val	Lys	Val 745	Asp	Val	Thr	Gly	Ala 750	Tyr	Asp
Thr	Ile	Pro 755	Gln	Asp	Arg	Leu	Thr 760	Glu	Val	Ile	Ala	Ser 765	Ile	Ile	Lys
Pro	Gln 770	Asn	Thr	Tyr	Cys	Val 775	Arg	Arg	Tyr	Ala	Val 780	Val	Gln	Lys	Ala
Ala 785	His	Gly	His	Val	Arg 790	Lys	Ala	Phe	Lys	Ser 795	His	Val	Ser	Thr	Leu 800
Thr	Asp	Leu	Gln	Pro 805	Tyr	Met	Arg	Gln	Phe 810	Val	Ala	His	Leu	Gln 815	Glu
Thr	Ser	Pro	Leu 820	Arg	Asp	Ala	Val	Val 825	Ile	Glu	Gln	Ser	Ser 830	Ser	Leu
Asn	Glu	Ala 835	Ser	Ser	Gly	Leu	Phe 840	Asp	Val	Phe	Leu	Arg 845	Phe	Met	Суѕ
His	His 850	Ala	Val	Arg	Ile	Arg 855	Gly	Lys	Ser	Tyr	Val 860	Gln	Cys	Gln	Gly
Ile 865	Pro	Gln	Gly	Ser	Ile 870	Leu	Ser	Thr	Leu	Leu 875	Cys	Ser	Leu	Суз	Tyr 880
Gly	Asp	Met	Glu	Asn 885	Lys	Leu	Phe	Ala	Gly 890	Ile	Arg	Arg	Asp	Gly 895	Leu
Leu	Leu	Arg	Leu 900	Val	Asp	Asp	Phe	Leu 905	Leu	Val	Thr	Pro	His 910	Leu	Thr
His	Ala	Lys 915	Thr	Phe	Leu	Arg	Thr 920	Leu	Val	Arg	Gly	Val 925	Pro	Glu	Tyr
Gly	Cys 930	Val	Val	Asn	Leu	Arg 935	Lys	Thr	Val	Val	Asn 940	Phe	Pro	Val	Glu
Asp 945	Glu	Ala	Leu	Gly	Gly 950	Thr	Ala	Phe	Val	Gln 955	Met	Pro	Ala	His	Gly 960
Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val

965 970 975

Gln Ser Asp Tyr Ser Arg 980

<210> 71 <211> 3466 <212> DNA <213> Homo sapiens <220> <223> Altered C-Terminus Protein (ver.2); with Introns Y, Alpha, Beta and 3

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tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc agtggcctct 2520
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<210> 72
<211> 1130
<212> PRT
<213> Homo sapiens
<220>
<223> Altered C-Terminus Protein (ver.2); encoded by SEQ
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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                              40
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
      50
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
                                 105
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
                             120
         115
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
                                              140
                         135
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
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                      150
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Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 175 165
Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 180 185
Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro 205
Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 210 220
Ser Gly Pro Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 240
Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 255 245
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 260 265
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 285 275
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 290 295
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 320 315 320
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gin 335
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 340
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu 370 380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 390 395 400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 420
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 445 435
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 450 450

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Asp Thr Asp Pro Arg 480 470
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 495 485
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 500 500
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 535 540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 550 555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu 11e Leu Ard 575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 590 580
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg 620 610
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val 640 625
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg 655 650 655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr 670 660
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu 685 675
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala 690 695
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile 720 715 705
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gin Asp F10 735
Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp 740 745
Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys 765 755

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala 775
Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu 795 790
785 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu 815 805
Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Leu 830
Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys 840
His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly 855
Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr 880 875 865
Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu 895
Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr 910 900
His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 920
Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu
Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala Nic 960
945 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 975 965

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 1040 1025 1030 ...

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp 1060 1065 Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro 1095

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu 1125

<210> 73

<211> 1045

<212> PRT

<213> Homo sapiens

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ ID NO:71 with Intron Y ORF2 after the termination codon

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 150

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Gly Gly Ser 165

Ala	Ser	Arg	Ser 180	Leu	Pro	Leu	Pro	Lys 185	Arg	Pro	Arg	Arg	190	Ala	НІА
Pro	Glu	Pro 195	Glu	Arg	Thr	Pro	Val 200	Gly	Gln	Gly	Ser	Trp 205	Ala	His	Pro
Gly	Arg 210	Thr	Arg	Gly	Pro	Ser 215	Asp	Arg	Gly	Phe	Cys 220	Val	Val	Ser	Pro
Ala 225	Arg	Pro	Ala	Glu	Glu 230	Ala	Thr	Ser	Leu	Glu 235	Gly	Ala	Leu	Ser	Gly 240
Thr	Arg	His	Ser	His 245	Pro	Ser	Val	Gly	Arg 250	Gln	His	His	Ala	Gly 255	Pro
Pro	Ser	Thr	Ser 260	Arg	Pro	Pro	Arg	Pro 265	Trp	Asp	Thr	Pro	Cys 270	Pro	Pro
Val	Tyr	Ala 275		ı Thr	Lys	His	Phe 280	Leu	Tyr	Ser	Ser	Gly 285	Asp	Lys	Glu
Gln	Leu 290	Arg	g Pro	o Ser	Phe	Leu 295	Leu	Ser	Ser	Leu	Arg 300	Pro	Ser	Leu	Thr
Gly 305		a Ar	g Ar	g Leu	val 310	. Glu	Thr	Ile	Phe	Leu 315	ı Gly	ser Ser	Arg	Pro	Trp 320
Met	Pro	G1	y Th	r Pro 325	Arç	g Arg	, Leu	Pro	330	Leu)	ı Pro	Glr	n Arg	335	Trp
			34	0				34.							Cys
Pro	о Ту:	r Gl 35	y Va 5	l Le	u Lei	Lys د	360	His	s Су:	s Pro	o Let	a Ard 36	g Ala 5	a Ala	val
Th	r Pr	o Al 0	a Al	a Gl	y Va	1 Cys 37	s Ala 5	a Ar	g Gli	ı Ly	s Pro	o Gl: 0	n Gly	y Sei	: Val
Al 38		a Pr	:o G1	.u Gl	u Gl 39	u Asj 0	p Th:	r As	p Pr	o Ar 39	g Ar	g Le	u Va	l Glı	1 Leu 400
Le	u Ar	g Gl	Ln Hi	is Se	r Se	r Pr	o Tr	p Gl	n Va 41	1 Ту 0	r Gl	y Ph	e Va	1 Ar	g Ala 5
Су	s Le	eu Ai	rg Ai	rg Le 20	eu Va	l Pr	o Pr	o Gl 42	y Le 5	u Tr	p Gl	y Se	er Ar 43	g Hi O	s Asn
Gl	u Ar	g A:	rg Pl 35	he Le	eu Ar	g As	n Th	r Ly O	s Ly	s Ph	ne Il	.e Se 44	er Le 15	u Gl	y Lys
Hi		la L 50	ys L	eu Se	er L€	eu Gl 45	n Gl	u Le	eu Th	r Tr	rp Ly 46	/s M∈ 50	et Se	er Va	l Arg
	sp Cy	ys A	la T	rp L	eu Ai 41	ng Ar 10	rg S∈	er Pr	o Gl	Ly Va 4	al G] 75	Ly C	ys Va	al Pr	o Ala 480

Ala	Glu	His	Arg	Leu 485	Arg	Glu	Glu	Ile	Leu 490	Ala	Lys	Phe	Leu	His 495	Trp
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Thr	Glu	Thr 515	Thr	Phe	Gln	Lys	Asn 520	Arg	Leu	Phe	Phe	Tyr 525	Arg	Lys	Ser
Val	Trp 530	Ser	Lys	Leu	Gln	Ser 535	Ile	Gly	Ile	Arg	Gln 540	His	Leu	Lys	Arg
Val 545	Gln	Leu	Arg	Glu	Leu 550	Ser	Glu	Ala	Glu	Val 555	Arg	Gln	His	Arg	Glu 560
Ala	Arg	Pro	Ala	Leu 565	Leu	Thr	Ser	Arg	Leu 570	Arg	Phe	Ile	Pro	Lys 575	Pro
Asp	Gly	Leu	Arg 580	Pro	Ile	Val	Asn	Met 585	Asp	Tyr	Val	Val	Gly 590	Ala	Arg
Thr	Phe	Arg 595	Arg	Glu	Lys	Arg	Ala 600	Glu	Arg	Leu	Thr	Ser 605	Arg	Val	Lys
Ala	Leu 610	Phe	Ser	Val	Leu	Asn 615	Tyr	Glu	Arg	Ala	Arg 620	Arg	Pro	Gly	Leu
Leu 625	Gly	Ala	Ser	Val	Leu 630	Gly	Leu	Asp	Asp	Ile 635	His	Arg	Ala	Trp	Arg 640
Thr	Phe	Val	Leu	Arg 645	Val	Arg	Ala	Gln	Asp 650	Pro	Pro	Pro	Glu	Leu 655	Tyr
Phe	Val	Lys	Val 660	Asp	Val	Thr	Gly	Ala 665	Tyr	Asp	Thr	Ile	Pro 670	Gln	Asp
Arg	Leu	Thr 675	Glu	Val	Ile	Ala	Ser 680	Ile	Ile	Lys	Pro	Gln 685	Asn	Thr	Tyr
Cys	Val 690	Arg	Arg	Tyr	Ala	Val 695	Val	Gln	Lys	Ala	Ala 700	His	Gly	His	Val
Arg 705	Lys	Ala	Phe	Lys	Ser 710	His	Val	Ser	Thr	Leu 715	Tḥr	Asp	Leu	Gln	Pro 720
Tyr	Met	Arg	Gln	Phe 725	Val	Ala	His	Leu	Gln 730	Glu	Thr	Ser	Pro	Leu 735	Arg
Asp	Ala	Val	Val 740	Ile	Glu	Gln	Ser	Ser 745	Ser	Leu	Asn	Glu	Ala 750	Ser	Ser
Gly	Leu	Phe 755	Asp	Val	Phe	Leu	Arg 760	Phe	Met	Cys	His	His 765	Ala	Val	Arg
Ile	Arg 770	Gly	Lys	Ser	Tyr	Val 775	Gln	Cys	Gln	Gly	Ile 780	Pro	Gln	Gly	Ser

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn 785 790 795 800

Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val 805 810 815

Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe 820 825 830

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn 835 840 845

Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly 850 860

Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys 865 870 875 880

Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser 885 890 895

Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly 900 905 910

Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg 915 920 925

Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln 930 935 940

Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln Ala Tyr Arg 945 950 955 960

Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys

Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys 980 985 990

Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val

Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro 1010 1015 1020

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Val Gly Leu Gly Leu 1045

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Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
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Ser	Gly 370		Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420		Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435		Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450		a Ala	u Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465		n Gly	y Sei	. Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arç	g Lei	ı Val	l Glr	n Leu 485	ı Lev	ı Arç	g Glr	n His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gl	y Phe	e Vai	1 Arg		a Cys	Leu	a Arg	g Arg 505	g Leu	ı Val	. Pro	Pro	Gly 510	Leu)	Trp
Gl	y Se	r Ar		s Ası	n Glu	ı Arç	9 Arc 520	g Phe	e Lei	a Arg	g Asn	Thi 525	Lys 5	s Lys	s Phe
11	e Se 53		u Gl	у Гу	s His	s Ala 53!	a Lys 5	s Lei	ı Sei	Let	1 Glr 540	ı Glu	ı Leı	ı Thi	Trp
Ly 54		t Se	r Va	l Ar	g Ası 55	o Cy: O	s Ala	a Tr	o Lei	a Arc 55	g Arq	g Sei	r Pro	o Gly	y Val 560
Gl	у Су	s Va	l Pr	o Al 56	a Al. 5	a Gl	u Hi	s Ar	g Lei 57	u Aro	g Glı	ı Gl	u Il	e Lei 57.	ı Ala 5

Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu : 590	Leu 1	Arg
Ser	Phe	Phe 595	Tyr	Val	Thr	Glu	Thr 600	Thr	Phe	Gln	Lys	Asn 605	Arg	Leu	Phe
Phe	Tyr 610	Arg	Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620	Ile	Gly	Ile	Arg
Gln 625	His	Leu	Lys	Arg	Val 630	Gln	Leu	Arg	Glu	Leu 635	Ser	Glu	Ala	Glu	Val 640
Arg	Gln	His	Arg	Glu 645	Ala	Arg	Pro	Ala	Leu 650	Leu	Thr	Ser	Arg	Leu 655	Arg
Phe	Ile	Pro	Lys 660	Pro	Asp	Gly	Leu	Arg 665	Pro	Ile	Val	Asn	Met 670	Asp	Tyr
Val	Val	Gly 675	Ala	Arg	Thr	Phe	Arg 680	Arg	Glu	Lys	Arg	Ala 685	Glu	Arg	Leu
Thr	Ser 690		Val	Lys	Ala	Leu 695	Phe	Ser	Val	Leu	Asn 700	Tyr	Glu	Arg	Ala
Arg 705		Pro	Gly	Leu	Leu 710	Gly	Ala	Ser	Val	Leu 715	Gly	Leu	Asp	Asp	Ile 720
His	Arg	Ala	Trp	Arg 725	Thr	Phe	Val	Leu	Arg 730	Val	Arg	Ala	Gln	Asp 735	Pro
Pro	Pro	Glu	1 Leu 740	Tyr	Phe	Val	Lys	Val 745	Asp	Val	Thr	Gly	Ala 750	Tyr	Asp
Thr	Ile	Pro 755	Glr	n Asp	Arg	Leu	Thr 760	Glu	Val	Ile	Ala	Ser 765	Ile	Ile	Lys
Pro	Glr 770		n Thi	Tyr	Cys	Val 775	Arg	Arg	Tyr	Ala	Val 780	Val	. Gln	Lys	Ala
Ala 785	a His	s Gl	y His	s Val	Arg 790	Lys	s Ala	Phe	e Lys	Ser 795	His	Val	Ser	Thr	Leu 800
Thi	c Asp	Le	u Gli	n Pro 809	о Туг 5 .	Met	: Arc	g Glr	n Phe 810	e Val	Ala	His	s Leu	Gln 815	Glu
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Ası	n Gl	u Al 83	a Se. 5	r Se	r Gly	y Lei	a Phe 840	e Asp	o Vai	l Phe	e Lei	a Arg 845	g Ph€ 5	e Met	: Cys
Hi	s Hi 85	s Al O	a Va	l Ar	g Il	e Arc 85	g Gly 5	y Ly	s Se:	r Ty:	r Val	l Gli	n Cys	s Glr	n Gly
I1 86		o Gl	n Gl	y Se	r Il	e Le	u Se	r Th	r Le	u Lei 87	и Су: 5	s Se	r Le	л Су:	880

Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu 885 890 895

Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr 915 920 925

Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu 930 935 940

Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly 945 950 955 960

Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 965 970 975

Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu 980 985 990

Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu 995 1000 1005

Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln 1010 1015 1020

Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 1025 1030 1035 1040

Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His 1045 1050 1055

Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu 1125 1130

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<220>

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	ancatogogg	ccaccacgtc	cctgggacac	goottgroce	ccygigiacy	1080
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	aacacaacac	- cccaacctcc	- Eddacacacac	LULUCLYYY	Ceggaegaea	
tecacadade	ctaacacacc	ttcatactac	. qtqtqcqggc	ccaygacccy	ccgcccgago	
+ ~+ ~ ~+ + + ~+	caaddacadd	-crcacddadd	Lualuquuay	Cattattaa	CCCCagaaa	
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	- aaaaaatatat	-accttdacau	acciccauce	, utacatycya	cagecogogg	
		- caactaaaaa	aracca: ca.	Calcuaucau	agetee	
+ +	- andended	-crcrrcoaco	i i.C.L.C.C.Lacc	CCCCCCGCGCGC	caccacges	
	at agagget a	tactacaaca	i aca uuauaa	Laauctuses	qcqqqqacc	
	+ + +	$-2\alpha\alpha2CCCCCC$	i i ccaaaa a	. CCCCGGGGGG	9900909099	
+~~~~++~~~	. ~~~~~~~~	ardaaci icc	: L.L.u.Lauaauc	i Çquqqccccq	999999	
	~~+~~~~~~~~	$-\alpha$ actactcca	i acialocaca	, uacciccate	uququuu	
tracetteaa	. ccacaacttc	aaddctuuud	i ggaacatge	Cogcadacco	~~~	7 1
+~~~~~+~~	. <u>atatasasaa</u> a	CEGELLCIO	ı attıtucaddı	, qaacaqccc		
~~~~~~~	· atagagata	- ctcctactac	. addcdtacac	i dilicacidea	Lytytyttyt	. 5120
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Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly 65 70 75 80	
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu 85 90 95	
Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys	
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Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly 130 135 140	
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr 145 150 155 160	
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg 165 170 175	

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Phe	Val	Leu 195	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205	Gly	Pro	Pro
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Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
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Arg	Arg	Gly 275		Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290		His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
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Thr	Pro	Cys 355	Pro) Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
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Gly	/ Sei	c Arg	g Pro	7rp	Met	Pro	Gly	7 Thr	Pro 410	Arç	Arq	g Lei	ı Pro	415	Leu S
Pro	o Glr	n Arg	g Ty:		Glr	n Met	Arg	g Pro 425	Leu 5	ı Phe	e Let	ı Glu	1 Let 430	ı Leu	ı Gly
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Lei	u Are		a Ala	a Vai	l Thi	r Pro 45	o Ala	a Ala	a Gl	y Val	1 Cy:	s Ala	a Aro	g Glı	ı Lys
Pr:		n Gl	y Se	r Vai	1 Ala	a Ala	a Pro	o Gli	u Gl	u Gli 47	u Ası	p Th	r Ası	o Pro	Arç 480

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Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu 590	Leu	Arg
Ser	Phe	Phe 595		Val	Thr	Glu	Thr 600	Thr	Phe	Gln	Lys	Asn 605	Arg	Leu	Phe
Phe	Tyr 610		Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620	Ile	Gly	Ile	Arg
625)				630					055	,				Val 640
				645)				650	,					
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		67	5				681)				003	,		J Leu
	691	0				69)				700	,			g Ala
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Se	r Il	e Il 75		s Pr	o Gl	n As	n Th 76	r Ту 0	r Cy	s Va	l Ar	g Ar 76	д Ту 5	r Al	a Val
Va	.1 Gl 77		s Al	a Al	a Hi	s Gl 77	у Ні 5	s Va	l Ar	g Ly	s Al 78	a Ph O	e Ly	s Se	r His

Val Ser 5	Thr Leu	Thr Asp		Gln	Pro	Tyr	Met 795	Arg	Gln	Phe	Val	Ala 800
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Arg Phe 1	Met Cys 835	His His	Ala	Val 840	Arg	Ile	Arg	Gly	Lys 845	Ser	Tyr	Val
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Arg Asp (Gly Leu	Leu Leu 885	ı Arg	Leu	Val	Asp 890	Asp	Phe	Leu	Leu	Val 895	Thr
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Pro Ala I 945	His Gly	Leu Phe 950		Trp	Cys	Gly	Leu 955	Leu	Leu	Asp	Thr	Arg 960
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Arg Ala S	Ser Leu 980	Thr Phe	. Asn	Arg	Gly 985	Phe	Lys	Ala	Gly	Arg 990	Asn	Met
Arg Arg	Lys Leu 995	Phe Gly		Leu 1000	Arg	Leu	Lys		His 1005	Ser	Leu	Phe
Leu Asp 1	Leu Gln	Val Asr	Ser 1015	Leu	Gln	Thr		Cys 1020	Thr	Asn	Ile	Tyr
Lys Ile 1 1025	Leu Leu	Leu Glr 1030		Tyr	Arg		His 1035	Ala	Cys	Val		Gln l040
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Val Ile S	Ser Asp 1060	Thr Ala	Ser		Cys 1065	Tyr	Ser	Ile		Lys 1070	Ala	Lys
Asn Ala (Gly Met 075	Ser Le		Ala 1080	Lys	Gly	Ala		Gly 1085	Pro	Leu	Pro

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu 1090 1095 1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr 1105 1110 1115 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala 1125 1130 1135

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Leu Asp

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Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly 145 150 155 160

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Pro	Glu	Pro 195	Glu	Arg	Thr	Pro	Val 200	Gly	Gln	Gly	Ser	Trp 205	Ala	His	Pro
Gly	Arg 210	Thr	Arg	Gly	Pro	Ser 215	Asp	Arg	Gly	Phe	Cys 220	Val	Val	Ser	Pro
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Glr	n Met	Ar	g Pro 340	Leu	ı Ph∈	e Leu	(Glu	Leu 345	Leu 5	ı Gly	Asn	His	Ala 350	Gln	Cys
Pro	о Туз	c Gl ₃	y Val	l Lei	ı Lev	ı Lys	360	His	s Cys	s Pro	Leu	365	Ala	Ala	Val
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Al 38		a Pr	o Gl	u Glı	u Gli 390	ı Asp	o Thi	As _l	p Pro	o Aro	g Aro	y Let	ı Val	. Glr	Leu 400
Le	u Ar	g Gl	n Hi	s Se 40	r Se: 5	r Pr	o Trj	Gl:	n Va 41	1 Ty:	r Gly	y Phe	e Val	415	g Ala
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Gl	u Ar	g Ar 43	g Ph	e Le	u Ar	g As	n Th 44	r Ly O	s Ly	s Ph	e Il	e Se 44	r Lei 5	ı Gl	y Lys
Hi	s Al 45	a Ly 50	/s Le	u Se	r Le	u Gl 45	n Gl 5	u Le	u Th	r Tr	р Ly 46	s Me O	t Se	r Va	l Arg

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Ala	Glu	His	Arg	Leu 485	Arg	Glu	Glu	Ile	Leu 490	Ala	Lys	Phe	Leu	His 495	Trp
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Thr	Glu	Thr 515	Thr	Phe	Gln	Lys	Asn 520	Arg	Leu	Phe	Phe	Tyr 525	Arg	Lys	Ser
Val	Trp 530	Ser	Lys	Leu	Gln	Ser 535	Ile	Gly	Ile	Arg	Gln 540	His	Leu	Lys	Arg
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Asp	Gly	Leu	Arg 580	Pro	Ile	Val	Asn	Met 585	Asp	Tyr	Val	Val	Gly 590	Ala	Arg
Thr	Phe	Arg 595		Glu	Lys	Arg	Ala 600	Glu	Arg	Leu	Thr	Ser 605	Arg	Val	Lys
Ala	Leu 610		Ser	Val	Leu	Asn 615	Tyr	Glu	Arg	Ala	Arg 620	Arg	Pro	Gly	Leu
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Gln	Asn	Thr 675		Cys	Val	Arg	Arg 680	Tyr	Ala	Val	Val	Gln 685	Lys	Ala	Ala
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Ser	Pro	Let	ı Arç	725		a Val	Val	. Ile	730	ı Glm	Ser	Ser	Ser	735	Asn
Glı	ı Ala	a Sei	740		/ Let	ı Phe	e Asp	745	L Ph∈	e Leu	ı Arg	Phe	Met 750	Cys	His
His	s Ala	a Val 75!		g Ile	e Arg	g Gly	7 Lys 760	s Ser	с Туі	r Val	. Gln	Cys 765	Glr	n Gly	, Ile

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Ala	Lys	Thr	Phe 820	Leu	Arg	Thr	Leu	Val 825	Arg	Gly	Val	Pro	Glu 830	Tyr	Gly
Cys	Val	Val 835	Asn	Leu	Arg	Lys	Thr 840	Val	Val	Asn	Phe	Pro 845	Val	Glu	Asp
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Phe 865		Trp	Cys	Gly	Leu 870	Leu	Leu	Asp	Thr	Arg 875	Thr	Leu	Glu	Val	Gln 880
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Gly	val	Leu 915	ı Arg	Leu	Lys	Cys	His 920	Ser	Leu	Phe	Leu	Asp 925	Leu	Gln	Val
Asr	Ser 930		ı Gln	Thr	· Val	. Cys 935	Thr	Asn	ıle	е Туг	Lys 940	: Ile	e Leu	Leu	Leu
Glr 945		а Туз	r Arg	, Phe	950	s Ala	a Cys	. Val	. Le	ı Glr 955	Leu 5	ı Pro	Phe	His	Gln 960
Glr	n Val	l Trj	o Lys	8 Asr 969	n Pro	Thi	r Phe	e Ph€	e Let 970	a Arg	g Val	L Il∈	e Ser	975	Thr
Ala	a Se:	r Le	u Cys 980	з Ту: Э	r Sei	c Ile	e Lei	Lys 985	s Ala	a Lys	s Ası	n Ala	a Gly 990	y Met	Ser
Le	u Gl	y Al 99	a Ly: 5	s Gl	y Ala	a Ala	a Gly	y Pro	o Le	u Pr	o Se	r Gli 100	u Ala 5	a Val	L Gln
Tr	р Le 101		s Hi	s Gl	n Ala	a Ph 101	e Le	u Le	u Ly	s Le	u Th:	r Ar	g Hi:	s Ar	g Val
	r Ty 25	r Va	l Pr	o Le	u Le 103	u Gl O	y Se	r Le	u Ar	g Th 103	r Al 5	a Gl	n Th	r Gl	n Leu 1040
Se	r Ar	g Ly	s Le	u Pr 104	o Gl 5	y Th	r Th	r Le	u Th	r Al	a Le	u Gl	u Al	a Al 105	a Ala 5

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Ala	Leu 50		Ala	Gln	Cys	Le 5	u '	Val	Cys	Val	Pr	0 7	rp 60	Asp	Ala	Arg	Pro
Pro 65		Ala	Ala	Pro	Sei 70	r Ph	ne .	Arg	Gln	Val	Pr	o 1	Pro	Arg	Gly	Arg	Arg 80
	Ala	Gly	. Val	. Glu 85	Gl:	y G	Lу	Arg	Gly	Glu 90	ı Pr	0 2	Ala	Thr	Cys	Gly 95	Glu
Gln	Arg	Arg	J Arg	j Lei		g A	la	Leu	Pro	Pro	o GI	ln	Val	Ser	Cys 110	Leu	Lys
Glu	Leu	Val	L Ala		g Va	1 L	eu	Gln 120	Arg	Le	a C	ys	Glu	Arg 125	Gly	Ala	Lys
Asn	Val	Lei		a Ph	e Gl	у Р 1	he 35	Ala	Lev	ı Le	u A	sp	Gly 140	Ala	Arg	g Gly	, Gly
Pro 145	Pro		u Al	a Ph	e Th	r T	hr	Ser	· Val	L Ar	g S 1	er 55	Туг	Leu	ı Pro	Ası	160
		c As	p Al	a Le 16	u Ar 5	:g 0	Sly	Sei	Gl	y Al 17	а Т О	rp	Gly	, Le	ı Leı	Leı 17	ı Arg 5
Arg	y Val	l Gl	y As	p As		al I	ieu	Va:	l Hi 18	s Le 5	eu I	eu	Ala	a Àr	g Cy:	s Al	a Leu
Ph∈	e Va	l Le 19	u Va		.a P	ro S	Ser	Cy:	s Al O	a Ty	r (Sln	Va.	1 Cy 20	s Gl 5	y Pr	o Pro
Le	Ту 21	r Gl		eu Gl	Ly A	la i	Ala 215	Th	r Gl	n Al	la A	٩rg	Pr 22	o Pr O	o Pr	o Hi	s Ala
Se:	r Gl		co A:	rg A	rg A 2	rg 30	Leı	ı Gl	у Су	rs G	lu 2	Arg 235	Al	a Tr	p As	n Hi	s Sei 240

Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg

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Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
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Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
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Ile	Ser 530		Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
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Thr	Ser 690		y Val	Lys	s Ala	Leu 695	Phe	Ser	Va:	l Lei	Ası 700	n Tyr	Glu	a Arg	g Al	a
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Aı	rg Ph	ne Me	et Cy 35	ys Hi	is Hi	s Al	.a Va 84	al A:	rg I	le A	rg G	ly Ly 84	ys Se 45	er T	yr V	/al
G.	In Ci	ıs Gi	ln G	ly I	le Pı	co Gl	ln G	Ly S	er I	le L	eu S	er Tl	hr L	eu L	eu (Cys

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Se	r Il	e Il 75	e Ly	s Pr	o Gl	n Ası	n Th:	r Ty	r Cy	s Va	l Ar	g Ar 76	g Ty: 5	r Ala	a Val
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				260)					20	J			Th:						
		2	275						201	,				r Se						
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G1 30		la .	Arg	Ar	g Lė	eu V	al (10	Glu	Th	r Il	e E	?he	Le 31	u Gl 5	y Se	er A	rg	Pro	32	р !0
					32	25					•	,,,		u Pr						
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T	hr F	ro	Ala	a Al	La G	ly V	'al	Суз	s Al	a A	rg	Glu	ı Ly	s P	ro G	ln (Sly	Se	r V	al

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Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln

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His	Arg	Ala	Trp	Arg 725	Thr	Phe	Val	Leu	Arg 730	Val	Arg	Ala	Gln	Asp 735	Pro
Pro	Pro	Glu	Leu 740	Tyr	Phe	Val	Lys	Asp 745	Arg	Leu	Thr	Glu	Val 750	Ile	Ala
		755	5	Pro			160								
Val	Gln 770	Lys	s Alá	a Ala	His	Gly 775	His	Val	Arg	l Lys	780	Phe	Lys	Ser	His
785	•				790)				150	,				Ala 800
				805)				010	J					Gln
			82	0				023)				• -		e Leu
		83	5				841	J				-	•		Val
Glı	n Cy 85		n Gl	y Il	e Pro	o Gli 85	n Gly 5	y Se	r Il	e Le	u Sei 860	r Th:	r Le	ı Lev	ı Cys
86	5				87	U				0 /	•				e Arg 880
Ar	g As	p Gl	Ly Le	eu Le 88	u Le 5	u Ar	g Le	u Va	1 As 89	p As	p Ph	e Le	u Le	u Va:	l Thr 5
Pr	o Hi	s Le	eu Th 90	nr Hi 00	s Al	a Ly	s Th	r Ph 90	e Le 15	eu Ar	g Th	r Le	u Va 91	1 Ar 0	g Gly
Va	ıl Pr		lu Ty 15	yr Gl	.у Су	s Va	ıl Va 92	1 As	n L∈	eu Ar	g Ly	s Th 92	ır Va 25	l Va	l Asn
Ph		co Va	al G	lu As	sp Gl	u Al 93	.a Le 35	eu Gl	Ly Gl	Ly Th	nr Al 94	.a Ph 10	ne Va	ıl Gl	n Met

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Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg
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<212> DNA
<213> Homo sapiens
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<223> Protein Lacking Motif A and Altered C-Terminus
      (ver.2); with Intron Y, Beta and 3
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gacgcacgge cgccccccgc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
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gggcccgcgg gggcccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540
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gcgcctacca ggtgtgcggg ccgccgctgt accagctcgg cgctgccact caggcccggc 660
ccccgccaca cgctagtgga ccccgaaggc gtctgggatg cgaacgggcc tggaaccata 720
gcgtcaggga ggccggggtc cccctgggcc tgccagcccc gggtgcgagg aggcgcgggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggcccag gcgtggcgct gcccctgagc 840
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gtgaccgtgg tttctgtgtg gtgtcacctg ccagacccgc cgaagaagcc acctctttgg 960
agggtgcgct ctctggcacg cgccactccc acccatccgt gggccgccag caccacgcgg 1020
gcccccatc cacatcgcgg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080
ccgagaccaa gcactteete taeteeteag gcgacaagga gcagetgegg cccteettee 1140
tactcagete tetgaggeee ageetgactg gegeteggag getegtggag accatettte 1200
tgggttccag gccctggatg ccagggactc cccgcaggtt gccccgcctg ccccagcgct 1260
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gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920
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agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100
actacgageg ggegeggege eeeggeetee tgggegeete tgtgetggge etggaegata 2160
tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220
tgtactttgt caaggacagg ctcacggagg tcatcgccag catcatcaaa ccccagaaca 2280
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cqtactqcqt qcqtcqqtat qccqtgqtcc agaaggccgc ccatgggcac gtccgcaagg 2340

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tgaatgagge cagcagtgge etettegacg tetteetacg etteatgtge caccaegeeg 2520
tgcgcatcag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
ccacgetget etgeageetg tgetaeggeg acatggagaa caagetgttt geggggatte 2640
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acacggcctc cctctgctac tccatcctga aagccaagaa cgcagccgaa gaaaacattt 3240
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cgtcgggtgt gggcagcttt ccggtgtctc ctgggagggg agttgggctg ggcctgtgac 3360
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      (ver.2); encoded by SEQ ID NO:83 with Intron Y
      ORF1
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
                             40
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
                         55
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
 65
Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
                                105
            100
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
                            120
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
                        135
    130
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Pro 145	Pro	Glu	Ala	Phe	Thr 150	Thr	Ser	Val	Arg	Ser 155	Tyr	Leu	Pro	Asn	Thr 160
Val	Thr	Asp	Ala	Leu 165	Arg	Gly	Ser	Gly	Ala 170	Trp	Gly	Leu	Leu	Leu 175	Arg
Arg	Val	Gly	Asp 180	Asp	Val	Leu	Val	His 185	Leu	Leu	Ala	Arg	Cys 190	Ala	Leu
Phe	Val	Leu 195	Val	Ala	Pro	Ser	Cys 200	Ala	Tyr	Gln	Val	Cys 205	Gly	Pro	Pro
Leu	Tyr 210	Gln	Leu	Gly	Ala	Ala 215	Thr	Gln	Ala	Arg	Pro 220	Pro	Pro	His	Ala
Ser 225	Gly	Pro	Arg	Arg	Arg 230	Leu	Gly	Cys	Glu	Arg 235	Ala	Trp	Asn	His	Ser 240
Val	Arg	Glu	Ala	Gly 245	Val	Pro	Leu	Gly	Leu 250	Pro	Ala	Pro	Gly	Ala 255	Arg
Arg	Arg	Gly	Gly 260	Ser	Ala	Ser	Arg	Ser 265	Leu	Pro	Leu	Pro	Lys 270	Arg	Pro
Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290		His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305		Val	. Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Let	ı Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	s Ala	Gly 340) Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	350	Trp	Asp
Thr	Pro	Cys 355	s Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe	e Leu	Tyr	Ser
Ser	Gl ₂		p Lys	Glu	ı Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	ı Ser	Ser	Leu
Arg 385		o Se:	r Lei	ı Thi	Gly 390	y Ala	a Arg	Arg	J Leu	ı Val 395	Glu	Thi	c Il€	e Ph∈	400
Gly	y Se:	r Ar	g Pro	o Tri 40	o Met	: Pro	Gly	7 Thr	Pro 410	Arg	y Arg	Lev	ı Pro	Arç 415	g Leu
Pro	o Gli	n Ar	g Ty:		o Glr	n Met	: Arq	g Pro 425	Let	ı Phe	e Lev	ı Glı	u Lei 430	ı Leu	ı Gly
Ası	n Hi	s Al 43		n Cy	s Pro	о Туг	c Gly 440	y Vai	l Lei	ı Leı	ı Lys	Th:	r Hi: 5	s Су:	s Pro

Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys 545	Met	Ser	Val	Arg	Asp 550	Cys	Ala	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560
Gly	Cys	Val	Pro	Ala 565	Ala	Glu	His	Arg	Leu 570	Arg	Glu	Glu	Ile	Leu 575	Ala
Lys	Phe	Leu	His 580	Trp	Leu	Met	Ser	Val 585	Tyr	Val	Val	Glu	Leu 590	Leu	Arg
Ser	Phe	Phe 595	Tyr	Val	Thr	Glu	Thr 600	Thr	Phe	Gln	Lys	Asn 605	Arg	Leu	Phe
Phe	Tyr 610		l Lys	Ser	Val	Trp 615	Ser	Lys	Leu	Gln	Ser 620	Ile	Gly	Ile	Arg
Gln 625		Leu	ı Lys	s Arg	Val 630	Gln	Leu	Arg	Glu	Leu 635	Ser	Glu	Ala	Glu	Val 640
Arg	g Glr	n His	s Arg	g Glu 645	a Ala	Arg	g Pro	Ala	Leu 650	Leu)	Thr	Ser	Arg	Leu 655	Arg
Ph∈	e Ile	e Pro	660	s Pro	Asp	Gly	, Lev	Arç 665	Pro	o Ile	e Val	Asr	Met 670	Asp	Tyr
Va]	L Vai	l Gl:	y Ala	a Aro	g Thi	: Phe	e Arc	Arc	g Glu	ı Lys	s Arg	Ala 685	a Glu 5	ı Arç	, Leù
Thi	Se:		g Vai	l Ly:	s Ala	Le: 69!	ı Phe 5	e Sei	val	l Lei	1 Asr 700	туз)	r Glı	ı Arç	g Ala
Ar 70		g Pr	o Gl	y Le	u Lei 710	ı Gl	y Ala	a Sei	r Vai	1 Let 71!	ı Gly 5	, Le	u Asp	Asp	720
Hi	s Ar	g Al	a Tr	p Ar 72	g Thi	r Ph	e Va	l Lei	a Aro 73	g Val	l Ar	g Ala	a Gl	n Ası 73!	Pro
Pr	o Pr	o Gl	u Le 74		r Ph	e Va	l Ly	s As _] 74	p Ar	g Le	u Thi	r Gl	u Va 75	1 Il	e Ala

Ser	Ile	Ile 755	Lys	Pro	Gln	Asn	Thr 760	Tyr	Cys	Val	Arg	Arg 7 6 5	Tyr	Ala	Val
Val	Gln 770	Lys	Ala	Ala	His	Gly 775	His	Val	Arg	Lys	Ala 780	Phe	Lys	Ser	His
Val 785	Ser	Thr	Leu	Thr	Asp 790	Leu	Gln	Pro	Tyr	Met 795	Arg	Gln	Phe	Val	Ala 800
His	Leu	Gln	Glu	Thr 805	Ser	Pro	Leu	Arg	Asp 810	Ala	Val	Val	Ile	Glu 815	Gln
Ser	Ser	Ser	Leu 820	Asn	Glu	Ala	Ser	Ser 825	Gly	Leu	Phe	Asp	Val 830	Phe	Leu
Arg	Phe	Met 835	Cys	His	His	Ala	Val 840	Arg	Ile	Arg	Gly	Lys 845	Ser	Tyr	Val
Gln	Cys 850	Gln	Gly	Ile	Pro	Gln 855	Gly	Ser	Ile	Leu	Ser 860	Thr	Leu	Leu	Cys
Ser 865	Leu	Cys	Tyr	Gly	Asp 870	Met	Glu	Asn	Lys	Leu 875	Phe	Ala	Gly	Ile	Arg 880
Arg	Asp	Gly	Leu	Leu 885	Leu	Arg	Leu	Val	Asp 890	Asp	Phe	Leu	Leu	Val 895	Thr
Pro	His	Leu	Thr 900	His	Ala	Lys	Thr	Phe 905	Leu	Arg	Thr	Leu	Val 910	Arg	Gly
Val	Pro	Glu 915	Tyr	Gly	Cys	Val	Val 920	Asn	Leu	a Arg	Lys	Thr 925	Val	Val	Asn
Phe	Pro 930		Glu	ı Asp	Glu	Ala 935	Leu	Gly	Gly	7 Thr	940	Phe	val	Gln	Met
Pro 945		His	s Gly	/ Leu	Phe 950	e Pro	Trp	Суз	Gly	/ Leu 955	ı Lev	ı Lev	a Asp	Thr	Arg 960
Thr	Leu	ı Glı	ı Val	L Glr 965	ser	Asp	туг	Ser	Ser 970	г Туг Э	: Ala	a Arç	g Thr	Ser 975	Ile
Arg	g _. Ala	a Se:	r Lei 980	ı Thi	r Ph∈	e Asr	n Arg	985 985	y Ph∈ 5	e Lys	s Alá	a Gly	990	g Asr)	n Met
Arg	g Arq	g Ly: 99		u Phe	e Gly	y Val	Let 1000	ı Ar	g Lei	u Lys	з Суя	s His	s Sei 5	Let	ı Phe
Lei	As ₁		u Glı	n Val	l Ası	n Se:	r Lei	ı Glı	n Th	r Va	1 Cy:	s Thi	r Ası	n Ile	e Tyr
Ly:		e Le	u Lei	u Lei	u Gla 103	n Ala	а Ту	r Ar	g Ph	e Hi 103	s Al	а Су	s Val	l Lei	u Gln 1040
Le	u Pr	o Ph	e Hi	s Gl:	n Gl: 5	n Va	l Tr	р Гу	s As 105	n Pr O	o Th	r Ph	e Ph	e Le	u Arç 5

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1060

Asn Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly 1080

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly 1100 1095 1090

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile 1105

Gly Ala

<210> 85

<211> 1037

<212> PRT

<213> Homo sapiens

<220>

<223> Protein Lacking Motif A and Altered C-Terminus (ver.2); encoded by SEQ ID NO:83 with Intron Y ORF2 after the termination codon

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg 20

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu

Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val Gly Asp Asp

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala 105

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly 125 115

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly

Val	Pro	Leu	G1	у L	eu I 65	?ro	Ala	Pro	G]	Ly .	Ala 170	Ar	g	Arg	Arg	ſ G.	ly	Gly 175	Se	r
Ala	Ser	Arg	Se 18	r L O	eu I	Pro	Leu	Pro	L; 18	ys 85	Arg	Pi	ro	Arg	Arç	ј G 1	ly 90	Ala	A]	.a
Pro	Glu	Pro 195	G1	u A	rg '	Thr	Pro	Val 200	G	ly	Gln	G.	ly	Ser	Trp 205	р А 5	.la	His	Pı	0
Gly	Arg 210	Thr	Ar	g G	Sly	Pro	Ser 215	Asp	A	rg	Gly	P	he	Cys 220	Va.	1 V	al	Ser	P:	ro
Ala 225	Arg	Pro) A]	La G	Glu	Glu 230	Ala	Thr	: S	er	Lev	ı G 2	1u 35	Gly	Al	a I	_eu	Ser	G 2	ly 40
Thr	Arg	His	s Se	er H	His 245	Pro	Ser	Va]	LG	Sly	Arg 250	g G	ln	His	Hi	s A	Ala	Gly 255	P	ro
Pro	Ser	Thi	r S	er <i>1</i> 60	Arg	Pro	Pro	Arg	g E	Pro 265	Tr	o P	Asp	Thr	Pr	· o (Cys 270	Pro) P	ro
Val	Tyr	Al: 27	a G 5	l.u '	Thr	Lys	His	28	e I O	Leu	Ту	r S	Ser	Sei	G1 28	.у 2 35	Asp	Lys	3 0	lu
	Let 290)					293)						-						
305						310)						J 1 0							
	: Pro				325						5.	, ,								
	n Me			340						54.	,									
	о Ту	35	55					3 (30											
	r Pr 37	0					31	5						-						
38						39	U						0,5	•						
					40	5					-1	10								Ala
				420	ı					4 2										Asn
		4	35					4	40											Lys
H		la I 50	ys	Leu	ı Se	r Le	eu G 4	ln G 55	Slu	L€	eu T	hr	Tı	cp L 4	ys 60	Met	: S€	er V	al	Arg

Asp 465	Cys	Ala	Trp	Leu	Arg 470	Arg	Ser	Pro	Gly	Val 475	Gly	Cys	Val	Pro .	480
Ala	Glu	His	Arg	Leu 485	Arg	Glu	Glu	Ile	Leu 490	Ala	Lys	Phe	Leu	His 495	Trp
Leu	Met	Ser	Val 500	Tyr	Val	Val	Glu	Leu 505	Leu	Arg	Ser	Phe	Phe 510	Tyr	Val
Thr	Glu	Thr 515	Thr	Phe	Gln	Lys	Asn 520	Arg	Leu	Phe	Phe	Tyr 525	Arg	Lys	Ser
	530					535	Ile				510				
545					550		Glu			333					
				565			Ser		570						
			580)			Asn	202					-		
		595	5				Ala 600					• • •			
	610)				φ15)				020				Leu
625	5				630)				050	,				Arg 640
				64	5				050	,					
			66	0				00.)						s Pro
		67	5				001	,					-		a Ala
	69	0				69	5				, 0				ı Thr
70	5				/ 1	U				, 1	9				u Thr 720
Se	r Pr	o Le	eu Ar	g As	p Al 25	a Va	l Va	1 Il	e Gl 73	u Gl 80	n Se	r Se	r Se	r Le	u Asn 5
			74	10				/ 4							s His
Ні	s Al	ia Va 7!	al Ai 55	rg Il	le Ar	g Gl	Lу Lу 76	s Se	er Ty	/r Va	al Gl	n Cy 76	s Gl 5	n Gl	y Ile

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly 770 780

Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu 785 790 795

Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His 805 810 815

Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly 820 825 830

Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp 835

Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu 850 855

Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln 865 870 875

Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr 885 890 895

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe 900 905 910

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val 915 920 925

Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu 930 935 940

Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln 945 950 955 960

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr 965 970 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu 980 985 990

Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu 995 1000 1005

Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser 1010 1015 1020

Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile Gly Ala 1025 1030 1035

<210> 86

<211> 1122

<212> PRT

<213> Homo sapiens

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Pro
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Amplification Primer Design based on EST Sequence GenBank Accession Number AA281296

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Amplification Primer Design based on EST Sequence
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        Amplification Primer Design Kased on EST Sequence
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                                                                        23
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38

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  His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu
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Gln Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
                            120
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
                                        155
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
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165 170 175 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu 185 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala 215 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser 235 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg 250 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro 265 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly 280 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe 295 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu 310 315 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln 335 325 330 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp 345 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser 355 360 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu 385 395 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu 410 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly 420 425 430 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro 440 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys 455 450 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg



465 470 475 480 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr 490 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp 505 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe 520 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cos Ala Trp Leu Arg Arg Ser Pro Gly Val 555 Gly Cys Val Pro Ala Ala Glu Hi Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 585 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gun Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly